

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

(A) NAME: Pasteur Merieux serums et vaccins
(B) STREET: 58, avenue leclerc
(C) CITY: Lyons
(E) COUNTRY: France
(F) POSTAL CODE: 69007

(A) NAME: Transgene
(B) STREET: 11, rue de Molsheim
(C) CITY: Strasbourg
(E) COUNTRY: France
(F) POSTAL CODE: 67000

(ii) TITLE OF INVENTION: Tbp2 fragments of N. meningitidis

(iii) NUMBER OF SEQUENCES: 35

(iv) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Tape
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25
(EPO)

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2230 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Neisseria meningitidis
(B) STRAIN: IM2169

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 60..119

(ix) FEATURE:

(A) NAME/KEY: mat_peptide
(B) LOCATION: 120..2192

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 60..2192

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION: 120..1154

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION: 1155..1748

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION: 1749..2192

(ix) FEATURE:

(A) NAME/KEY: misc_binding
(B) LOCATION: 127..1169

(x1) SEQUENCE DESCRIPTION : SEQ ID NO: 1:

ATTGTTAAA AATAAATAAA ATAATAATCC TTATCATTCT TTAATTGAAT TGGGTTTAT 59
 ATG AAC AAT CCA TTG GTA AAT CAG GCT GCT ATG GTG CTG CCT GTG TTT 107
 Met Asn Asn Pro Leu Val Asn Gln Ala Ala Met Val Leu Pro Val Phe
 -20 -15 -10 -5
 TTG TTG AGT GCC TGT CTG GGC GGC GGC GGC AGT TTC GAT CTT GAT TCT 155
 Leu Leu Ser Ala Cys Leu Gly Gly Gly Gly Ser Phe Asp Leu Asp Ser
 1 5 10
 GTC GAT ACC GAA GCC CCG CGT CCC GCG CCA AAG TAT CAA GAT GTT TCT 203
 Val Asp Thr Glu Ala Pro Arg Pro Ala Pro Lys Tyr Gln Asp Val Ser
 15 20 25
 TCC GAA AAA CCG CAA GCC CAA AAA GAC CAA GGC GGA TAC GGT TTT GCG 251
 Ser Glu Lys Pro Gln Ala Gln Lys Asp Gln Gly Gly Tyr Gly Phe Ala
 30 35 40
 ATG AGG TTG AAA CGG AGG AAT TGG TAT CCG GGG GCA GAA GAA AGC GAG 299
 Met Arg Leu Lys Arg Arg Asn Trp Tyr Pro Gly Ala Glu Glu Ser Glu
 45 50 55 60
 GTT AAA CTG AAC GAG AGT GAT TGG GAG GCG ACG GGA TTG CCG ACA AAA 347
 Val Lys Leu Asn Glu Ser Asp Trp Glu Ala Thr Gly Leu Pro Thr Lys
 65 70 75
 CCC AAG GAA CTT CCT AAA CGG CAA AAA TCG GTT ATT GAA AAA GTA GAA 395
 Pro Lys Glu Leu Pro Lys Arg Gln Lys Ser Val Ile Glu Lys Val Glu
 80 85 90
 ACA GAC GGC GAC AGC GAT ATT TAT TCT TCC CCC TAT CTC ACA CCA TCA 443
 Thr Asp Gly Asp Ser Asp Ile Tyr Ser Ser Pro Tyr Leu Thr Pro Ser
 95 100 105
 AAC CAT CAA AAC GGC AGC GCT GGC AAC GGT GTA AAT CAA CCT AAA AAT 491
 Asn His Gln Asn Gly Ser Ala Gly Asn Gly Val Asn Gln Pro Lys Asn
 110 115 120
 CAG GCA ACA GGT CAC GAA AAT TTC CAA TAT GTT TAT TCC GGT TGG TTT 539
 Gln Ala Thr Gly His Glu Asn Phe Gln Tyr Val Tyr Ser Gly Trp Phe
 125 130 135 140
 TAT AAA CAT GCA GCG AGT GAA AAA GAT TTC AGT AAC AAA AAA ATT AAG 587
 Tyr Lys His Ala Ala Ser Glu Lys Asp Phe Ser Asn Lys Lys Ile Lys
 145 150 155
 TCA GGC GAC GAT GGT TAT ATC TTC TAT CAC GGT GAA AAA CCT TCC CGA 635
 Ser Gly Asp Asp Gly Tyr Ile Phe Tyr His Gly Glu Lys Pro Ser Arg
 160 165 170
 CAA CTT CCT GCT TCT GGA AAA GTT ATC TAC AAA GGT GTG TGG CAT TTT 683
 Gln Leu Pro Ala Ser Gly Lys Val Ile Tyr Lys Gly Val Trp His Phe
 175 180 185

GTA ACC GAT ACA AAA AAG GGT CAA GAT TTT CGT GAA ATT ATC CAG CCT Val Thr Asp Thr Lys Lys Gly Gln Asp Phe Arg Glu Ile Ile Gln Pro 190 195 200	731
TCA AAA AAA CAA GGC GAC AGG TAT AGC GGA TTT TCT GGT GAT GGC AGC Ser Lys Lys Gln Gly Asp Arg Tyr Ser Gly Phe Ser Gly Asp Gly Ser 205 210 215 220	779
GAA GAA TAT TCC AAC AAA AAC GAA TCC ACG CTG AAA GAT GAT CAC GAG Glu Glu Tyr Ser Asn Lys Asn Glu Ser Thr Leu Lys Asp Asp His Glu 225 230 235	827
GGT TAT GGT TTT ACC TCG AAT TTA GAA GTG GAT TTC GGC AAT AAG AAA Gly Tyr Gly Phe Thr Ser Asn Leu Glu Val Asp Phe Gly Asn Lys Lys 240 245 250	875
TTG ACG GGT AAA TTA ATA CGC AAT AAT GCG AGC CTA AAT AAT AAT ACT Leu Thr Gly Lys Leu Ile Arg Asn Asn Ala Ser Leu Asn Asn Asn Thr 255 260 265	923
AAT AAT GAC AAA CAT ACC ACC CAA TAC TAC AGC CTT GAT GCA CAA ATA Asn Asn Asp Lys His Thr Thr Gln Tyr Tyr Ser Leu Asp Ala Gln Ile 270 275 280	971
ACA GGC AAC CGC TTC AAC GGC ACG GCA ACG GCA ACT GAC AAA AAA GAG Thr Gly Asn Arg Phe Asn Gly Thr Ala Thr Ala Thr Asp Lys Lys Glu 285 290 295 300	1019
AAT GAA ACC AAA CTA CAT CCG TTT GTT TCC GAC TCG TCT TCT TTG AGC Asn Glu Thr Lys Leu His Pro Phe Val Ser Asp Ser Ser Ser Leu Ser 305 310 315	1067
GGC GGC TTT TTC GGC CCG CAG GGT GAG GAA TTG GGT TTC CGC TTT TTG Gly Gly Phe Phe Gly Pro Gln Gly Glu Glu Leu Gly Phe Arg Phe Leu 320 325 330	1115
AGC GAC GAT CAA AAA GTT GCC GTT GTC GGC AGC GCG AAA ACC AAA GAC Ser Asp Asp Gln Lys Val Ala Val Val Gly Ser Ala Lys Thr Lys Asp 335 340 345	1163
AAA CTG GAA AAT GGC GCG GCG GCT TCA GGC AGC ACA GGT GCG GCA GCA Lys Leu Glu Asn Gly Ala Ala Ala Ser Gly Ser Thr Gly Ala Ala Ala 350 355 360	1211
TCG GGC GGT GCG GCA GGC ACG TCG TCT GAA AAC AGT AAG CTG ACC ACG Ser Gly Gly Ala Ala Gly Thr Ser Ser Glu Asn Ser Lys Leu Thr Thr 365 370 375 380	1259
GTT TTG GAT GCG GTT GAA TTG ACA CTA AAC GAC AAG AAA ATC AAA AAT Val Leu Asp Ala Val Glu Leu Thr Leu Asn Asp Lys Lys Ile Lys Asn 385 390 395	1307
CTC GAC AAC TTC AGC AAT GCC GCC CAA CTG GTT GTC GAC GGC ATT ATG Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu Val Val Asp Gly Ile Met 400 405 410	1355
ATT CCG CTC CTG CCC AAG GAT TCC GAA AGC GGG AAC ACT CAG GCA GAT Ile Pro Leu Leu Pro Lys Asp Ser Glu Ser Gly Asn Thr Gln Ala Asp 415 420 425	1403
AAA GGT AAA AAC GGC GGA ACA GAA TTT ACC CGC AAA TTT GAA CAC ACG Lys Gly Lys Asn Gly Gly Thr Glu Phe Thr Arg Lys Phe Glu His Thr 430 435 440	1451

CCG GAA AGT GAT AAA AAA GAC GCC CAA GCA GGT ACG CAG ACG AAT GGG Pro Glu Ser Asp Lys Lys Asp Ala Gln Ala Gly Thr Gln Thr Asn Gly 445 450 455 460	1499
GCG CAA ACC GCT TCA AAT ACG GCA GGT GAT ACC AAT GGC AAA ACA AAA Ala Gln Thr Ala Ser Asn Thr Ala Gly Asp Thr Asn Gly Lys Thr Lys 465 470 475	1547
ACC TAT GAA GTC GAA GTC TGC TGT TCC AAC CTC AAT TAT CTG AAA TAC Thr Tyr Glu Val Glu Val Cys Cys Ser Asn Leu Asn Tyr Leu Lys Tyr 480 485 490	1595
GGA ATG TTG ACG CGC AAA AAC AGC AAG TCC GCG ATG CAG GCA GGA GGA Gly Met Leu Thr Arg Lys Asn Ser Lys Ser Ala Met Gln Ala Gly Gly 495 500 505	1643
AAC AGT AGT CAA GCT GAT GCT AAA ACG GAA CAA GTT GAA CAA AGT ATG Asn Ser Ser Gln Ala Asp Ala Lys Thr Glu Gln Val Glu Gln Ser Met 510 515 520	1691
TTC CTC CAA GGC GAG CGT ACC GAT GAA AAA GAG ATT CCA ACC GAC CAA Phe Leu Gln Gly Glu Arg Thr Asp Glu Lys Glu Ile Pro Thr Asp Gln 525 530 535 540	1739
AAC GTC GTT TAT CGG GGG TCT TGG TAC GGG CAT ATT GCC AAC GGC ACA Asn Val Val Tyr Arg Gly Ser Trp Tyr Gly His Ile Ala Asn Gly Thr 545 550 555	1787
AGC TGG AGC GGC AAT GCT TCT GAT AAA GAG GGC GGC AAC AGG GCG GAA Ser Trp Ser Gly Asn Ala Ser Asp Lys Glu Gly Gly Asn Arg Ala Glu 560 565 570	1835
TTT ACT GTG AAT TTT GCC GAT AAA AAA ATT ACC GGC AAG TTA ACC GCT Phe Thr Val Asn Phe Ala Asp Lys Lys Ile Thr Gly Lys Leu Thr Ala 575 580 585	1883
GAA AAC AGG CAG GCG CAA ACC TTT ACC ATT GAG GGA ATG ATT CAG GGC Glu Asn Arg Gln Ala Gln Thr Phe Thr Ile Glu Gly Met Ile Gln Gly 590 595 600	1931
AAC GGC TTT GAA GGT ACG GCG AAA ACT GCT GAG TCA GGT TTT GAT CTC Asn Gly Phe Glu Gly Thr Ala Lys Thr Ala Glu Ser Gly Phe Asp Leu 605 610 615 620	1979
GAT CAA AAA AAT ACC ACC CGC ACG CCT AAG GCA TAT ATC ACA GAT GCC Asp Gln Lys Asn Thr Thr Arg Thr Pro Lys Ala Tyr Ile Thr Asp Ala 625 630 635	2027
AAG GTA AAG GGC GGT TTT TAC GGG CCT AAA GCC GAA GAG TTG GGC GGA Lys Val Lys Gly Gly Phe Tyr Gly Pro Lys Ala Glu Glu Leu Gly Gly 640 645 650	2075
TGG TTT GCC TAT CCG GGC GAT AAA CAA ACG GAA AAG GCA ACA GCT ACA Trp Phe Ala Tyr Pro Gly Asp Lys Gln Thr Glu Lys Ala Thr Ala Thr 655 660 665	2123
TCC AGC GAT GGA AAT TCA GCA AGC AGC GCG ACC GTG GTA TTC GGT GCG Ser Ser Asp Gly Asn Ser Ala Ser Ser Ala Thr Val Val Phe Gly Ala 670 675 680	2171
AAA CGC CAA CAG CCT GTG CAA TAAGCACGGT TGCCGAACAA TCAAGAATAA Lys Arg Gln Gln Pro Val Gln 685 690	2222

GGCTTCAG

2230

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 711 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met Asn Asn Pro Leu Val Asn Gln Ala Ala Met Val Leu Pro Val Phe
-20 -15 -10 -5
Leu Leu Ser Ala Cys Leu Gly Gly Gly Gly Ser Phe Asp Leu Asp Ser
1 5 10
Val Asp Thr Glu Ala Pro Arg Pro Ala Pro Lys Tyr Gln Asp Val Ser
15 20 25
Ser Glu Lys Pro Gln Ala Gln Lys Asp Gln Gly Gly Tyr Gly Phe Ala
30 35 40
Met Arg Leu Lys Arg Arg Asn Trp Tyr Pro Gly Ala Glu Glu Ser Glu
45 50 55 60
Val Lys Leu Asn Glu Ser Asp Trp Glu Ala Thr Gly Leu Pro Thr Lys
65 70 75
Pro Lys Glu Leu Pro Lys Arg Gln Lys Ser Val Ile Glu Lys Val Glu
80 85 90
Thr Asp Gly Asp Ser Asp Ile Tyr Ser Ser Pro Tyr Leu Thr Pro Ser
95 100 105
Asn His Gln Asn Gly Ser Ala Gly Asn Gly Val Asn Gln Pro Lys Asn
110 115 120
Gln Ala Thr Gly His Glu Asn Phe Gln Tyr Val Tyr Ser Gly Trp Phe
125 130 135 140
Tyr Lys His Ala Ala Ser Glu Lys Asp Phe Ser Asn Lys Lys Ile Lys
145 150 155
Ser Gly Asp Asp Gly Tyr Ile Phe Tyr His Gly Glu Lys Pro Ser Arg
160 165 170
Gln Leu Pro Ala Ser Gly Lys Val Ile Tyr Lys Gly Val Trp His Phe
175 180 185
Val Thr Asp Thr Lys Lys Gly Gln Asp Phe Arg Glu Ile Ile Gln Pro
190 195 200
Ser Lys Lys Gln Gly Asp Arg Tyr Ser Gly Phe Ser Gly Asp Gly Ser
205 210 215 220
Glu Glu Tyr Ser Asn Lys Asn Glu Ser Thr Leu Lys Asp Asp His Glu
225 230 235

Gly Tyr Gly Phe Thr Ser Asn Leu Glu Val Asp Phe Gly Asn Lys Lys
 240 245 250
 Leu Thr Gly Lys Leu Ile Arg Asn Asn Ala Ser Leu Asn Asn Asn Thr
 255 260 265
 Asn Asn Asp Lys His Thr Thr Gln Tyr Tyr Ser Leu Asp Ala Gln Ile
 270 275 280
 Thr Gly Asn Arg Phe Asn Gly Thr Ala Thr Ala Thr Asp Lys Lys Glu
 285 290 295 300
 Asn Glu Thr Lys Leu His Pro Phe Val Ser Asp Ser Ser Ser Leu Ser
 305 310 315
 Gly Gly Phe Phe Gly Pro Gln Gly Glu Glu Leu Gly Phe Arg Phe Leu
 320 325 330
 Ser Asp Asp Gln Lys Val Ala Val Val Gly Ser Ala Lys Thr Lys Asp
 335 340 345
 Lys Leu Glu Asn Gly Ala Ala Ala Ser Gly Ser Thr Gly Ala Ala Ala
 350 355 360
 Ser Gly Gly Ala Ala Gly Thr Ser Ser Glu Asn Ser Lys Leu Thr Thr
 365 370 375 380
 Val Leu Asp Ala Val Glu Leu Thr Leu Asn Asp Lys Lys Ile Lys Asn
 385 390 395
 Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu Val Val Asp Gly Ile Met
 400 405 410
 Ile Pro Leu Leu Pro Lys Asp Ser Glu Ser Gly Asn Thr Gln Ala Asp
 415 420 425
 Lys Gly Lys Asn Gly Gly Thr Glu Phe Thr Arg Lys Phe Glu His Thr
 430 435 440
 Pro Glu Ser Asp Lys Lys Asp Ala Gln Ala Gly Thr Gln Thr Asn Gly
 445 450 455 460
 Ala Gln Thr Ala Ser Asn Thr Ala Gly Asp Thr Asn Gly Lys Thr Lys
 465 470 475
 Thr Tyr Glu Val Glu Val Cys Cys Ser Asn Leu Asn Tyr Leu Lys Tyr
 480 485 490
 Gly Met Leu Thr Arg Lys Asn Ser Lys Ser Ala Met Gln Ala Gly Gly
 495 500 505
 Asn Ser Ser Gln Ala Asp Ala Lys Thr Glu Gln Val Glu Gln Ser Met
 510 515 520
 Phe Leu Gln Gly Glu Arg Thr Asp Glu Lys Glu Ile Pro Thr Asp Gln
 525 530 535 540
 Asn Val Val Tyr Arg Gly Ser Trp Tyr Gly His Ile Ala Asn Gly Thr
 545 550 555
 Ser Trp Ser Gly Asn Ala Ser Asp Lys Glu Gly Gly Asn Arg Ala Glu
 560 565 570

Phe Thr Val Asn Phe Ala Asp Lys Lys Ile Thr Gly Lys Leu Thr Ala
 575 580 585
 Glu Asn Arg Gln Ala Gln Thr Phe Thr Ile Glu Gly Met Ile Gln Gly
 590 595 600
 Asn Gly Phe Glu Gly Thr Ala Lys Thr Ala Glu Ser Gly Phe Asp Leu
 605 610 615 620
 Asp Gln Lys Asn Thr Thr Arg Thr Pro Lys Ala Tyr Ile Thr Asp Ala
 625 630 635
 Lys Val Lys Gly Gly Phe Tyr Gly Pro Lys Ala Glu Glu Leu Gly Gly
 640 645 650
 Trp Phe Ala Tyr Pro Gly Asp Lys Gln Thr Glu Lys Ala Thr Ala Thr
 655 660 665
 Ser Ser Asp Gly Asn Ser Ala Ser Ser Ala Thr Val Val Phe Gly Ala
 670 675 680
 Lys Arg Gln Gln Pro Val Gln
 685 690

(2) INFORMATION FOR SEQ ID NO. 3:

- 5
- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1808 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- 10 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: N. meningitidis
 (B) STRAIN: IM2394
- (ix) FEATURE:
 (A) NAME/KEY: sig_peptide
 (B) LOCATION: 1..60
- 15 (ix) FEATURE:
 (A) NAME/KEY: mat_peptide
 (B) LOCATION: 61..1797
- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 1..1797
- 20 (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 61..1035
- 25 (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 1036..1386
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 1387..1797
- 30 (ix) FEATURE:
 (A) NAME/KEY: misc_binding
 (B) LOCATION: 46..1050

(xi) SEQUENCE DESCRIPTION : SEQ ID NO: 3:

ATG AAC AAT CCA TTG GTA AAT CAG GCT GCT ATG GTG CTG CCT GTG TTT Met Asn Asn Pro Leu Val Asn Gln Ala Ala Met Val Leu Pro Val Phe -20 -15 -10 -5	48
TTG TTG AGT GCT TGT CTG GGT GGC GGC GGC AGT TTC GAT TTG GAC AGC Leu Leu Ser Ala Cys Leu Gly Gly Gly Ser Phe Asp Leu Asp Ser 1 5 10	96
GTG GAA ACC GTG CAA GAT ATG CAC TCC AAA CCT AAG TAT GAG GAT GAA Val Glu Thr Val Gln Asp Met His Ser Lys Pro Lys Tyr Glu Asp Glu 15 20 25	144
AAA AGC CAG CCT GAA AGC CAA CAG GAT GTA TCG GAA AAC AGC GGC GCG Lys Ser Gln Pro Glu Ser Gln Gln Asp Val Ser Glu Asn Ser Gly Ala 30 35 40	192
GCT TAT GGC TTT GCA GTA AAA CTA CCT CGC CGG AAT GCA CAT TTT AAT Ala Tyr Gly Phe Ala Val Lys Leu Pro Arg Arg Asn Ala His Phe Asn 45 50 55 60	240
CCT AAA TAT AAG GAA AAG CAC AAA CCA TTG GGT TCA ATG GAT TCG AAA Pro Lys Tyr Lys Glu Lys His Lys Pro Leu Gly Ser Met Asp Trp Lys 65 70 75	288
AAA CTG CAA AGA GGA GAA CCA AAT AGT TTT AGT GAG AGG GAT GAA TTG Lys Leu Gln Arg Gly Glu Pro Asn Ser Phe Ser Glu Arg Asp Glu Leu 80 85 90	336
GAA AAA AAA CGG GGT AGT TCT GAA CTT ATT GAA TCA AAA TGG GAA GAT Glu Lys Lys Arg Gly Ser Ser Glu Leu Ile Glu Ser Lys Trp Glu Asp 95 100 105	384
GGG CAA AGT CGT GTA GTT GGT TAT ACA AAT TTC ACT TAT GTC CGT TCG Gly Gln Ser Arg Val Val Gly Tyr Thr Asn Phe Thr Tyr Val Arg Ser 110 115 120	432
GGA TAT GTT TAC CTT AAT AAA AAT AAT ATT GAT ATT AAG AAT AAT ATA Gly Tyr Val Tyr Leu Asn Lys Asn Asn Ile Asp Ile Lys Asn Asn Ile 125 130 135 140	480
GTT CTT TTT GGA CCT GAC GGA TAT CTT TAC TAT AAA GGG AAA GAA CCT Val Leu Phe Gly Pro Asp Gly Tyr Leu Tyr Tyr Lys Gly Lys Glu Pro 145 150 155	528
TCC AAG GAG CTG CCA TCG GAA AAG ATA ACT TAT AAA GGT ACT TGG GAT Ser Lys Glu Leu Pro Ser Glu Lys Ile Thr Tyr Lys Gly Thr Trp Asp 160 165 170	576
TAT GTT ACT GAT GCT ATG GAA AAA CAA AGG TTT GAA GGA TTG GGT AGT Tyr Val Thr Asp Ala Met Glu Lys Gln Arg Phe Glu Gly Leu Gly Ser 175 180 185	624
GCA GCA GGA GGA GAT AAA TCG GGG GCG TTG TCT GCA TTA GAA GAA GGG Ala Ala Gly Gly Asp Lys Ser Gly Ala Leu Ser Ala Leu Glu Glu Gly 190 195 200	672
GTA TTG CGT AAT CAG GCA GAG GCA TCA TCC GGT CAT ACC GAT TTT GGT Val Leu Arg Asn Gln Ala Glu Ala Ser Ser Gly His Thr Asp Phe Gly 205 210 215 220	720

ATG ACT AGT GAG TTT GAG GTT GAT TTT TCT GAT AAA ACA ATA AAG GGC Met Thr Ser Glu Phe Glu Val Asp Phe Ser Asp Lys Thr Ile Lys Gly 225 230 235	768
ACA CTT TAT CGT AAC AAC CGT ATT ACT CAA AAT AAT AGT GAA AAC AAA Thr Leu Tyr Arg Asn Asn Arg Ile Thr Gln Asn Asn Ser Glu Asn Lys 240 245 250	816
CAA ATA AAA ACT ACG CGT TAC ACC ATT CAA GCA ACT CTT CAC GGC AAC Gln Ile Lys Thr Thr Arg Tyr Thr Ile Gln Ala Thr Leu His Gly Asn 255 260 265	864
CGT TTC AAA GGT AAG GCG TTG GCG GCA GAT AAA GGT GCA ACA AAT GGA Arg Phe Lys Gly Lys Ala Leu Ala Ala Asp Lys Gly Ala Thr Asn Gly 270 275 280	912
AGT CAT CCC TTT ATT TCC GAC TCC GAC AGT TTG GAA GGC GGA TTT TAC Ser His Pro Phe Ile Ser Asp Ser Asp Ser Leu Glu Gly Gly Phe Tyr 285 290 295 300	960
GGG CCG AAA GGC GAG GAA CTT GCC GGT AAA TTC TTG AGC AAC GAC AAC Gly Pro Lys Gly Glu Glu Leu Ala Gly Lys Phe Leu Ser Asn Asp Asn 305 310 315	1008
AAA GTT GCA GCG GTG TTT GGT GCG AAG CAG AAA GAT AAG AAG GAT GGC Lys Val Ala Ala Val Phe Gly Ala Lys Gln Lys Asp Lys Lys Asp Gly 320 325 330	1056
GAA AAC GCG GCA GGG CCT GCA AAG GAA ACC GTG ATA GAT GCA TAC CGT Glu Asn Ala Ala Gly Pro Ala Thr Glu Thr Val Ile Asp Ala Tyr Arg 335 340 345	1104
ATT ACC GGC GAG GAG TTT AAG AAA GAG CAA ATA GAC AGT TTT GGA GAT Ile Thr Gly Glu Glu Phe Lys Lys Glu Gln Ile Asp Ser Phe Gly Asp 350 355 360	1152
GTG AAA AAG CTG CTG GTT GAC GGA GTG GAG CTT TCA CTG CTG CCG TCT Val Lys Lys Leu Leu Val Asp Gly Val Glu Leu Ser Leu Leu Pro Ser 365 370 375 380	1200
GAG GGC AAT AAG GCG GCA TTT CAG CAC GAG ATT GAG CAA AAC GGC GTG Glu Gly Asn Lys Ala Ala Phe Gln His Glu Ile Glu Gln Asn Gly Val 385 390 395	1248
AAG GCA ACG GTG TGT TGT TCC AAC TTG GAT TAC ATG AGT TTT GGG AAG Lys Ala Thr Val Cys Cys Ser Asn Leu Asp Tyr Met Ser Phe Gly Lys 400 405 410	1296
CTG TCA AAA GAA AAT AAA GAC GAT ATG TTC CTG CAA GGT GTC CGC ACT Leu Ser Lys Glu Asn Lys Asp Asp Met Phe Leu Gln Gly Val Arg Thr 415 420 425	1344
CCA GTA TCC GAT GTG GCG GCA AGG ACG GAG GCA AAC GCC AAA TAT CGC Pro Val Ser Asp Val Ala Ala Arg Thr Glu Ala Asn Ala Lys Tyr Arg 430 435 440	1392
GGT ACT TGG TAC GGA TAT ATT GCC AAC GGC ACA AGC TGG AGC GGC GAA Gly Thr Trp Tyr Gly Tyr Ile Ala Asn Gly Thr Ser Trp Ser Gly Glu 445 450 455 460	1440
GCC TCC AAT CAG GAA GGT GGT AAT AGG GCA GAG TTT GAC GTG GAT TTT Ala Ser Asn Gln Glu Gly Gly Asn Arg Ala Glu Phe Asp Val Asp Phe 465 470 475	1488

TCC ACT AAA AAA ATC AGT GGC ACA CTG ACG GCA AAA GAC CGT ACG TCT 1536
 Ser Thr Lys Lys Ile Ser Gly Thr Leu Thr Ala Lys Asp Arg Thr Ser
 480 485 490
 CCT GCG TTT ACT ATT ACT GCC ATG ATT AAG GAC AAC GGT TTT TCA GGT 1584
 Pro Ala Phe Thr Ile Thr Ala Met Ile Lys Asp Asn Gly Phe Ser Gly
 495 500 505
 GTG GCG AAA ACC GGT GAA AAC GGC TTT GCG CTG GAT CCG CAA AAT ACC 1632
 Val Ala Lys Thr Gly Glu Asn Gly Phe Ala Leu Asp Pro Gln Asn Thr
 510 515 520
 GGA AAT TCC CAC TAT ACG CAT ATT GAA GCC ACT GTA TCC GGC GGT TTC 1680
 Gly Asn Ser His Tyr Thr His Ile Glu Ala Thr Val Ser Gly Gly Phe
 525 530 535 540
 TAC GGC AAA AAC GCC ATC GAG ATG GGC GGA TCG TTC TCA TTT CCG GGA 1728
 Tyr Gly Lys Asn Ala Ile Glu Met Gly Gly Ser Phe Ser Phe Pro Gly
 545 550 555
 AAT GCA CCA GAG GGA AAA CAA GAA AAA GCA TCG GTG GTA TTC GGT GCG 1776
 Asn Ala Pro Glu Gly Lys Gln Glu Lys Ala Ser Val Val Phe Gly Ala
 560 565 570
 AAA CGC CAA CAG CTT GTG CAA TAAGCACGGC T 1808
 Lys Arg Gln Gln Leu Val Gln
 575

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 599 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Met Asn Asn Pro Leu Val Asn Gln Ala Ala Met Val Leu Pro Val Phe
 -20 -15 -10 -5
 Leu Leu Ser Ala Cys Leu Gly Gly Gly Gly Ser Phe Asp Leu Asp Ser
 1 5 10
 Val Glu Thr Val Gln Asp Met His Ser Lys Pro Lys Tyr Glu Asp Glu
 15 20 25
 Lys Ser Gln Pro Glu Ser Gln Gln Asp Val Ser Glu Asn Ser Gly Ala
 30 35 40
 Ala Tyr Gly Phe Ala Val Lys Leu Pro Arg Arg Asn Ala His Phe Asn
 45 50 55 60
 Pro Lys Tyr Lys Glu Lys His Lys Pro Leu Gly Ser Met Asp Trp Lys
 65 70 75
 Lys Leu Gln Arg Gly Glu Pro Asn Ser Phe Ser Glu Arg Asp Glu Leu
 80 85 90
 Glu Lys Lys Arg Gly Ser Ser Glu Leu Ile Glu Ser Lys Trp Glu Asp
 95 100 105

Gly Gln Ser Arg Val Val Gly Tyr Thr Asn Phe Thr Tyr Val Arg Ser
 110 115 120
 Gly Tyr Val Tyr Leu Asn Lys Asn Asn Ile Asp Ile Lys Asn Asn Ile
 125 130 135 140
 Val Leu Phe Gly Pro Asp Gly Tyr Leu Tyr Tyr Lys Gly Lys Glu Pro
 145 150 155
 Ser Lys Glu Leu Pro Ser Glu Lys Ile Thr Tyr Lys Gly Thr Trp Asp
 160 165 170
 Tyr Val Thr Asp Ala Met Glu Lys Gln Arg Phe Glu Gly Leu Gly Ser
 175 180 185
 Ala Ala Gly Gly Asp Lys Ser Gly Ala Leu Ser Ala Leu Glu Glu Gly
 190 195 200
 Val Leu Arg Asn Gln Ala Glu Ala Ser Ser Gly His Thr Asp Phe Gly
 205 210 215 220
 Met Thr Ser Glu Phe Glu Val Asp Phe Ser Asp Lys Thr Ile Lys Gly
 225 230 235
 Thr Leu Tyr Arg Asn Asn Arg Ile Thr Gln Asn Asn Ser Glu Asn Lys
 240 245 250
 Gln Ile Lys Thr Thr Arg Tyr Thr Ile Gln Ala Thr Leu His Gly Asn
 255 260 265
 Arg Phe Lys Gly Lys Ala Leu Ala Ala Asp Lys Gly Ala Thr Asn Gly
 270 275 280
 Ser His Pro Phe Ile Ser Asp Ser Asp Ser Leu Glu Gly Gly Phe Tyr
 285 290 295 300
 Gly Pro Lys Gly Glu Glu Leu Ala Gly Lys Phe Leu Ser Asn Asp Asn
 305 310 315
 Lys Val Ala Ala Val Phe Gly Ala Lys Gln Lys Asp Lys Lys Asp Gly
 320 325 330
 Glu Asn Ala Ala Gly Pro Ala Thr Glu Thr Val Ile Asp Ala Tyr Arg
 335 340 345
 Ile Thr Gly Glu Glu Phe Lys Lys Glu Gln Ile Asp Ser Phe Gly Asp
 350 355 360
 Val Lys Lys Leu Leu Val Asp Gly Val Glu Leu Ser Leu Leu Pro Ser
 365 370 375 380
 Glu Gly Asn Lys Ala Ala Phe Gln His Glu Ile Glu Gln Asn Gly Val
 385 390 395
 Lys Ala Thr Val Cys Cys Ser Asn Leu Asp Tyr Met Ser Phe Gly Lys
 400 405 410
 Leu Ser Lys Glu Asn Lys Asp Asp Met Phe Leu Gln Gly Val Arg Thr
 415 420 425
 Pro Val Ser Asp Val Ala Ala Arg Thr Glu Ala Asn Ala Lys Tyr Arg
 430 435 440

Gly Thr Trp Tyr Gly Tyr Ile Ala Asn Gly Thr Ser Trp Ser Gly Glu
 445 450 455 460
 Ala Ser Asn Gln Glu Gly Gly Asn Arg Ala Glu Phe Asp Val Asp Phe
 465 470 475
 Ser Thr Lys Lys Ile Ser Gly Thr Leu Thr Ala Lys Asp Arg Thr Ser
 480 485 490
 Pro Ala Phe Thr Ile Thr Ala Met Ile Lys Asp Asn Gly Phe Ser Gly
 495 500 505
 Val Ala Lys Thr Gly Glu Asn Gly Phe Ala Leu Asp Pro Gln Asn Thr
 510 515 520
 Gly Asn Ser His Tyr Thr His Ile Glu Ala Thr Val Ser Gly Gly Phe
 525 530 535 540
 Tyr Gly Lys Asn Ala Ile Glu Met Gly Gly Ser Phe Ser Phe Pro Gly
 545 550 555
 Asn Ala Pro Glu Gly Lys Gln Glu Lys Ala Ser Val Val Phe Gly Ala
 560 565 570

Lys Arg Gln Gln Leu Val Gln
575

(2) INFORMATION FOR SEQ ID NO: 5:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2255 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- 10 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: N. meningitidis
 (B) STRAIN: M978
- 15 (ix) FEATURE:
 (A) NAME/KEY: mat_peptide
 (B) LOCATION: 1..2115
- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 1..2115
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

TGT CTG GGT GGC GGC GGC ACG TTC GAT CTT GAT TCT GTC GAT ACC GAA 48
 Cys Leu Gly Gly Gly Thr Phe Asp Leu Asp Ser Val Asp Thr Glu
 1 5 10 15
 GCC CCG CGT CCC GCC CCA AAA TAT CAA GAT GTT TCT TCC GAA AAA CCG 96
 Ala Pro Arg Pro Ala Pro Lys Tyr Gln Asp Val Ser Ser Glu Lys Pro
 20 25 30
 CAA GCC CAA AAA GAC CAA GGC GGA TAC GGT TTT GCA ATG CGC CTC AAG 144
 Gln Ala Gln Lys Asp Gln Gly Gly Tyr Gly Phe Ala Met Arg Leu Lys
 35 40 45

CGG CGG AAT TGG CAT CCG CAG GCA AAT CCT AAA GAA GAT GAG ATA AAA	192
Arg Arg Asn Trp His Pro Gln Ala Asn Pro Lys Glu Asp Glu Ile Lys	
50 55 60	
CTT TCT GAA AAT GAT TGG GAG GCG ACA GGA TTG CCA GGC AAT CCC AAA	240
Leu Ser Glu Asn Asp Trp Glu Ala Thr Gly Leu Pro Gly Asn Pro Lys	
65 70 75 80	
AAC TTA CCT GAG CGA CAG AAA TCG GTT ATT GAA AAA GTA AAA ACA GGC	288
Asn Leu Pro Glu Arg Gln Lys Ser Val Ile Glu Lys Val Lys Thr Gly	
85 90 95	
AGC GAC AGC AAT ATT TAT TCT TCC CCC TAT CTC ACG CAA TCA AAC CAT	336
Ser Asp Ser Ile Tyr Ser Ser Pro Tyr Leu Thr Gln Ser Asn His	
100 105 110	
CAA AAC GGC AGT GCA AAC CAA CCA AAA AAT GAA GTA AAA GAT TAT AAA	384
Gln Asn Gly Ser Ala Asn Gln Pro Lys Asn Glu Val Lys Asp Tyr Lys	
115 120 125	
GAG TTC AAA TAT GTT TAT TCC GGT TGG TTT TAC AAA CAC GCT AAA CTC	432
Glu Phe Lys Tyr Val Tyr Ser Gly Trp Phe Tyr Lys His Ala Lys Leu	
130 135 140	
GAA ATC ATA AAA GAA AAC AAC TTA ATT AAG GGT GCA AAG AGC GGC GAC	480
Glu Ile Ile Lys Glu Asn Asn Leu Ile Lys Gly Ala Lys Ser Gly Asp	
145 150 155 160	
GAC GGT TAT ATC TTT TAT CAC GGT GAA AAA CCT TCC CGA CAA CTT CCC	528
Asp Gly Tyr Ile Phe Tyr His Gly Glu Lys Pro Ser Arg Gln Leu Pro	
165 170 175	
GTT TCT GGA GAA GTT ACC TAC AAA GGC GTA TGG CAT TTT GTA ACC GAT	576
Val Ser Gly Glu Val Thr Tyr Lys Gly Val Trp His Phe Val Thr Asp	
180 185 190	
ACG AAA CAG GGA CAA AAA TTT AAC GAT ATT CTT GGA ACC TCA AAA AAA	624
Thr Lys Gln Gly Gln Lys Phe Asn Asp Ile Leu Gly Thr Ser Lys Lys	
195 200 205	
CAA GGC GAC AGG TAT AGC GGA TTT CCG GGT GAT GAC GGC GAA GAA TAT	672
Gln Gly Asp Arg Tyr Ser Gly Phe Pro Gly Asp Asp Gly Glu Glu Tyr	
210 215 220	
TCC AAT AAA AAT GAA GCG ACT TTA CAA GGC AGT CAA GAG GGT TAT GGT	720
Ser Asn Lys Asn Glu Ala Thr Leu Gln Gly Ser Gln Glu Gly Tyr Gly	
225 230 235 240	
TTT ACC TCA AAT TTA AAA GTG GAT TTC AAT AAG AAA AAA TTG ACG GGT	768
Phe Thr Ser Asn Leu Lys Val Asp Phe Asn Lys Lys Lys Leu Thr Gly	
245 250 255	
GAA TTG ATA CGC AAT AAT AGA GTT ACA AAC GCT ACT GCT AAC GAT AAA	816
Glu Leu Ile Arg Asn Asn Arg Val Thr Asn Ala Thr Ala Asn Asp Lys	
260 265 270	
TAC ACC ACC CAA TAT TAC AGC CTT GAG GCT CAA GTA ACA GGC AAC CGC	864
Tyr Thr Thr Gln Tyr Tyr Ser Leu Glu Ala Gln Val Thr Gly Asn Arg	
275 280 285	
TTC AAC GGC AAG GCA ACG GCA ACC GAC AAA CCT GGC ACT GGA GAA ACC	912
Phe Asn Gly Lys Ala Thr Ala Thr Asp Lys Pro Gly Thr Gly Glu Thr	
290 295 300	

AAA CAA CAT CCC TTT GTT TCC GAC TCG TCT TCT TTG AGC GGC GGC TTT Lys Gln His Pro Phe Val Ser Asp Ser Ser Ser Leu Ser Gly Gly Phe 305 310 315 320	960
TTC GGC CCG AAG GGT GAG GAA TTG GGT TTC CGC TTT TTG AGC AAC GAT Phe Gly Pro Lys Gly Glu Glu Leu Gly Phe Arg Phe Leu Ser Asn Asp 325 330 335	1008
CAA AAA GTT GCC GTT GTC GGC AGC GCG AAA ACC CAA GAC AAA GCC GCA Gln Lys Val Ala Val Val Gly Ser Ala Lys Thr Gln Asp Lys Ala Ala 340 345 350	1056
AAT GGC AAT ACT GCG GCG GCT TCA GGC GGC ACA GAT GCG GCA GCA TCA Asn Gly Asn Thr Ala Ala Ala Ser Gly Gly Thr Asp Ala Ala Ala Ser 355 360 365	1104
AAC GGT GCG GCA GGC ACG TCG TCT GAA AAC AGT AAG CTG ACC ACG GTT Asn Gly Ala Ala Gly Thr Ser Ser Glu Asn Ser Lys Leu Thr Thr Val 370 375 380	1152
TTG GAT GCG GTT GAA TTG ACA CTA AAC GAC AAG AAA ATC AAA AAT CTC Leu Asp Ala Val Glu Leu Thr Leu Asn Asp Lys Lys Ile Lys Asn Leu 385 390 395 400	1200
GAC AAC TTC AGC AAT GCC GCC CAA CTG GTT GTC GAC GGC ATT ATG ATT Asp Asn Phe Ser Asn Ala Ala Gln Leu Val Val Asp Gly Ile Met Ile 405 410 415	1248
CCG CTC CTG CCC GAG ACT TCC GAA AGT GCG AGC AAT CAG GCA GAT AAA Pro Leu Leu Pro Glu Thr Ser Glu Ser Gly Ser Asn Gln Ala Asp Lys 420 425 430	1296
GGT AAA AAA GGT AAA AAC GGT AAA AAC GGC GGA ACA GAC TTT ACC TAC Gly Lys Lys Gly Lys Asn Gly Lys Asn Gly Gly Thr Asp Phe Thr Tyr 435 440 445	1344
AAA ACA ACC TAC ACG CCG AAA AAC GAT GAC AAA GAT ACC AAA GCC CAA Lys Thr Thr Tyr Thr Pro Lys Asn Asp Asp Lys Asp Thr Lys Ala Gln 450 455 460	1392
ACA GGT GCG GCA GGC TCT AGC GGC GCA CAA ACC GAT TTG GGT AAG GCG Thr Gly Ala Ala Gly Ser Ser Gly Ala Gln Thr Asp Leu Gly Lys Ala 465 470 475 480	1440
GAC GTT AAC GGC GGT AAG GCA GAA ACA AAA ACC TAT GAA GTC GAA GTC Asp Val Asn Gly Gly Lys Ala Glu Thr Lys Thr Tyr Glu Val Glu Val 485 490 495	1488
TGC TGT TCC AAC CTC AAT TAT CTG AAA TAC GGA ATG TTG ACG CGT AAA Cys Cys Ser Asn Leu Asn Tyr Leu Lys Tyr Gly Met Leu Thr Arg Lys 500 505 510	1536
AAC AGC AAG TCC GCG ATG CAG GCA GGA GGA AAC AGT AGT CAA GCT GAT Asn Ser Lys Ser Ala Met Gln Ala Gly Gly Asn Ser Ser Gln Ala Asp 515 520 525	1584
GCT AAA ACG GAA CAA GTT GAA CAA AGT ATG TTC CTC CAA GGC GAG CGT Ala Lys Thr Glu Gln Val Glu Gln Ser Met Phe Leu Gln Gly Glu Arg 530 535 540	1632
ACC GAT GAA AAA GAG ATT CCA AAC GAC CAA AAC GTC GTT TAT CGG GGG Thr Asp Glu Lys Glu Ile Pro Asn Asp Gln Asn Val Val Tyr Arg Gly 545 550 555 560	1680

TCT TGG TAC GGG CAT ATT GCC AGC AGC ACA AGC TGG AGC GGC AAT GCT 1728
 Ser Trp Tyr Gly His Ile Ala Ser Ser Thr Ser Trp Ser Gly Asn Ala
 565 570 575
 TCC AAT GCA ACG AGT GGC AAC AGG GCG GAA TTT ACT GTG AAT TTC GAT 1776
 Ser Asn Ala Thr Ser Gly Asn Arg Ala Glu Phe Thr Val Asn Phe Asp
 580 585 590
 ACG AAA AAA ATT AAC GGC ACG TTA ACC GCT GAA AAC AGG CAG GAG GCA 1824
 Thr Lys Lys Ile Asn Gly Thr Leu Thr Ala Glu Asn Arg Gln Glu Ala
 595 600 605
 ACC TTT ACC ATT GAT GGT AAG ATT GAG GGC AAC GGT TTT TCC GGT ACG 1872
 Thr Phe Thr Ile Asp Gly Lys Ile Glu Gly Asn Gly Phe Ser Gly Thr
 610 615 620
 GCA AAA ACT GCT GAC TTA GGT TTT GAT CTC GAT CAA AGC AAT ACC ACC 1920
 Ala Lys Thr Ala Asp Leu Gly Phe Asp Leu Asp Gln Ser Asn Thr Thr
 625 630 635 640
 GGC ACG CCT AAG GCA TAT ATC ACA GAT GCC AAG GTG CAG GGC GGT TTT 1968
 Gly Thr Pro Lys Ala Tyr Ile Thr Asp Ala Lys Val Gln Gly Gly Phe
 645 650 655
 TAC GGG CCT AAA GCC GAA GAG TTG GCC GGA TGG TTT GCC TAT CCG GGC 2016
 Tyr Gly Pro Lys Ala Glu Glu Leu Gly Gly Trp Phe Ala Tyr Pro Gly
 660 665 670
 GAT AAA CAA ACG GAA AAG GCA AAG GTT GCA TCC GGC GAT GGA AAT TCA 2064
 Asp Lys Gln Thr Glu Lys Ala Thr Val Ala Ser Gly Asp Gly Asn Ser
 675 680 685
 GCA AGC AGC GCG ACC GTG GTA TTC GGT GCG AAA CGC CAA CAG CCT GTG 2112
 Ala Ser Ser Ala Thr Val Phe Gly Ala Lys Arg Gln Gln Pro Val
 690 695 700
 CAA TAACTAAATG AAGTTGTCTG GGTGGCGGCG GCACGTTCTGA TCTTGATTCT 2165
 Gln
 705
 GTCGATACCG AAGCCCCGCG TCCCGCCCCA AAATATCAAG ATGTTTCTTC CGAAAAACCG 2225
 CAAGCCCCAAA AAGACCAAGG CGGATACGGT 2255

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 705 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Cys Leu Gly Gly Gly Gly Thr Phe Asp Leu Asp Ser Val Asp Thr Glu
 1 5 10 15
 Ala Pro Arg Pro Ala Pro Lys Tyr Gln Asp Val Ser Ser Glu Lys Pro
 20 25 30
 Gln Ala Gln Lys Asp Gln Gly Gly Tyr Gly Phe Ala Met Arg Leu Lys
 35 40 45

Arg Arg Asn Trp His Pro Gln Ala Asn Pro Lys Glu Asp Glu Ile Lys
 50 55 60
 Leu Ser Glu Asn Asp Trp Glu Ala Thr Gly Leu Pro Gly Asn Pro Lys
 65 70 75 80
 Asn Leu Pro Glu Arg Gln Lys Ser Val Ile Glu Lys Val Lys Thr Gly
 85 90 95
 Ser Asp Ser Asn Ile Tyr Ser Ser Pro Tyr Leu Thr Gln Ser Asn His
 100 105 110
 Gln Asn Gly Ser Ala Asn Gln Pro Lys Asn Glu Val Lys Asp Tyr Lys
 115 120 125
 Glu Phe Lys Tyr Val Tyr Ser Gly Trp Phe Tyr Lys His Ala Lys Leu
 130 135 140
 Glu Ile Ile Lys Glu Asn Asn Leu Ile Lys Gly Ala Lys Ser Gly Asp
 145 150 155 160
 Asp Gly Tyr Ile Phe Tyr His Gly Glu Lys Pro Ser Arg Gln Leu Pro
 165 170 175
 Val Ser Gly Glu Val Thr Tyr Lys Gly Val Trp His Phe Val Thr Asp
 180 185 190
 Thr Lys Gln Gly Gln Lys Phe Asn Asp Ile Leu Gly Thr Ser Lys Lys
 195 200 205
 Gln Gly Asp Arg Tyr Ser Gly Phe Pro Gly Asp Asp Gly Glu Glu Tyr
 210 215 220
 Ser Asn Lys Asn Glu Ala Thr Leu Gln Gly Ser Gln Glu Gly Tyr Gly
 225 230 235 240
 Phe Thr Ser Asn Leu Lys Val Asp Phe Asn Lys Lys Lys Leu Thr Gly
 245 250 255
 Glu Leu Ile Arg Asn Asn Arg Val Thr Asn Ala Thr Ala Asn Asp Lys
 260 265 270
 Tyr Thr Thr Gln Tyr Tyr Ser Leu Glu Ala Gln Val Thr Gly Asn Arg
 275 280 285
 Phe Asn Gly Lys Ala Thr Ala Thr Asp Lys Pro Gly Thr Gly Glu Thr
 290 295 300
 Lys Gln His Pro Phe Val Ser Asp Ser Ser Ser Leu Ser Gly Gly Phe
 305 310 315 320
 Phe Gly Pro Lys Gly Glu Glu Leu Gly Phe Arg Phe Leu Ser Asn Asp
 325 330 335
 Gln Lys Val Ala Val Val Gly Ser Ala Lys Thr Gln Asp Lys Ala Ala
 340 345 350
 Asn Gly Asn Thr Ala Ala Ala Ser Gly Gly Thr Asp Ala Ala Ala Ser
 355 360 365
 Asn Gly Ala Ala Gly Thr Ser Ser Glu Asn Ser Lys Leu Thr Thr Val
 370 375 380

Leu Asp Ala Val Glu Leu Thr Leu Asn Asp Lys Lys Ile Lys Asn Leu
385 390 395 400
Asp Asn Phe Ser Asn Ala Ala Gln Leu Val Val Asp Gly Ile Met Ile
405 410 415
Pro Leu Leu Pro Glu Thr Ser Glu Ser Gly Ser Asn Gln Ala Asp Lys
420 425 430
Gly Lys Lys Gly Lys Asn Gly Lys Asn Gly Gly Thr Asp Phe Thr Tyr
435 440 445
Lys Thr Thr Tyr Thr Pro Lys Asn Asp Asp Lys Asp Thr Lys Ala Gln
450 455 460
Thr Gly Ala Ala Gly Ser Ser Gly Ala Gln Thr Asp Leu Gly Lys Ala
465 470 475 480
Asp Val Asn Gly Gly Lys Ala Glu Thr Lys Thr Tyr Glu Val Glu Val
485 490 495
Cys Cys Ser Asn Leu Asn Tyr Leu Lys Tyr Gly Met Leu Thr Arg Lys
500 505 510
Asn Ser Lys Ser Ala Met Gln Ala Gly Gly Asn Ser Ser Gln Ala Asp
515 520 525
Ala Lys Thr Glu Gln Val Glu Gln Ser Met Phe Leu Gln Gly Glu Arg
530 535 540
Thr Asp Glu Lys Glu Ile Pro Asn Asp Gln Asn Val Val Tyr Arg Gly
545 550 555 560
Ser Trp Tyr Gly His Ile Ala Ser Ser Thr Ser Trp Ser Gly Asn Ala
565 570 575
Ser Asn Ala Thr Ser Gly Asn Arg Ala Glu Phe Thr Val Asn Phe Asp
580 585 590
Thr Lys Lys Ile Asn Gly Thr Leu Thr Ala Glu Asn Arg Gln Glu Ala
595 600 605
Thr Phe Thr Ile Asp Gly Lys Ile Glu Gly Asn Gly Phe Ser Gly Thr
610 615 620
Ala Lys Thr Ala Asp Leu Gly Phe Asp Leu Asp Gln Ser Asn Thr Thr
625 630 635 640
Gly Thr Pro Lys Ala Tyr Ile Thr Asp Ala Lys Val Gln Gly Gly Phe
645 650 655
Tyr Gly Pro Lys Ala Glu Glu Leu Gly Gly Trp Phe Ala Tyr Pro Gly
660 665 670
Asp Lys Gln Thr Glu Lys Ala Thr Val Ala Ser Gly Asp Gly Asn Ser
675 680 685
Ala Ser Ser Ala Thr Val Val Phe Gly Ala Lys Arg Gln Gln Pro Val
690 695 700
Gln
705

(2) INFORMATION FOR SEQ ID NO: 7:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2114 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: N. meningitidis
 (B) STRAIN: 6940
- (ix) FEATURE:
 (A) NAME/KEY: mat_peptide
 (B) LOCATION: 1..2079
- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 1..2079
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

TGT TTG GGT GGC GGC GGC ACG TTT GAT CTT GAT TCT GTC GAT ACC GAA	48
Cys Leu Gly Gly Gly Thr Phe Asp Leu Asp Ser Val Asp Thr Glu	
1 5 10 15	
GCC CCG CGT CCC GAC CCA AAG TAT CAA GAT GTT TCT TCC GAA AAA CCG	96
Ala Pro Arg Pro Asp Pro Lys Tyr Gln Asp Val Ser Ser Glu Lys Pro	
20 25 30	
CAA GCC CAA AAA GAC CAA GGC GGA TAC GGT TTT GCG ATG AGG TTG AAA	144
Gln Ala Gln Lys Asp Gln Gly Gly Tyr Gly Phe Ala Met Arg Leu Lys	
35 40 45	
CGG AGG AAT TGG TAT TCC GCA GCA AAA GAA GAC GAG GTT AAA CTG AAC	192
Arg Arg Asn Trp Tyr Ser Ala Ala Lys Glu Asp Glu Val Lys Leu Asn	
50 55 60	
GAG AGT GAT TGG GAG ACG ACA GGA TTG CCG ACA GAA CCC AAG AAA CTG	240
Glu Ser Asp Trp Glu Thr Thr Gly Leu Pro Thr Glu Pro Lys Lys Leu	
65 70 75 80	
CCA TTA AAA CAA GAA TCC GTC ATT TCA AAA GTA CAA GCA AAC AAT GGC	288
Pro Leu Lys Gln Glu Ser Val Ile Ser Lys Val Gln Ala Asn Asn Gly	
85 90 95	
GAC AAC AAT ATT TAC ACT TCC CCC TAT CTC ACG CAA TCA AAC CAT CAA	336
Asp Asn Asn Ile Tyr Thr Ser Pro Tyr Leu Thr Gln Ser Asn His Gln	
100 105 110	
AAT AGC AGC ATT AAT GGC GGT GCA AAC CTG CCA AAA AAC GAA GTA ACA	384
Asn Ser Ser Ile Asn Gly Gly Ala Asn Leu Pro Lys Asn Glu Val Thr	
115 120 125	
AAT TAT AAA GAT TTC AAA TAT GTT TAT TCC GGC TGG TTT TAT AAA CAT	432
Asn Tyr Lys Asp Phe Lys Tyr Val Tyr Ser Gly Trp Phe Tyr Lys His	
130 135 140	
GCT AAA AAC GAA ATC ATA AGA GAA AAC AGC TCA ATT AAG GGT GCA AAG	480
Ala Lys Asn Glu Ile Ile Arg Glu Asn Ser Ser Ile Lys Gly Ala Lys	
145 150 155 160	

AAC GGC GAC GAC GGC TAT ATC TTT TAT CAC GGC AAA GAA CCT TCC CGA Asn Gly Asp Asp Gly Tyr Ile Phe Tyr His Gly Lys Glu Pro Ser Arg 165 170 175	528
CAA CTT CCC GCT TCT GGA ACA GTT ACC TAT AAA GGT GTG TGG CAT TTT Gln Leu Pro Ala Ser Gly Thr Val Thr Tyr Lys Gly Val Trp His Phe 180 185 190	576
GCG ACC GAT GTC AAA AAA TCC CAA AAT TTT CGC GAT ATT ATC CAG CCT Ala Thr Asp Val Lys Lys Ser Gln Asn Phe Arg Asp Ile Ile Gln Pro 195 200 205	624
TCG AAA AAA CAA GGC GAC AGG TAT AGC GGA TTT TCG GGC GAT GAT GAT Ser Lys Lys Gln Gly Asp Arg Tyr Ser Gly Phe Ser Gly Asp Asp Asp 210 215 220	672
GAA CAA TAT TCT AAT AAA AAC GAA TCC ATG CTG AAA GAT GGT CAA GAG Glu Gln Tyr Ser Asn Lys Asn Glu Ser Met Leu Lys Asp Gly Gln Glu 225 230 235 240	720
GGT TAT GGT TTT ACC TCG AAT TTA GAA GTG GAT TTC GGC AGT AAA AAA Gly Tyr Gly Phe Thr Ser Asn Leu Glu Val Asp Phe Gly Ser Lys Lys 245 250 255	768
TTG ACG GGT AAA TTA ATA CGC AAT AAT AGA GTT ACA AAC GCT CCT ACT Leu Thr Gly Lys Leu Ile Arg Asn Asn Arg Val Thr Asn Ala Pro Thr 260 265 270	816
AAC GAT AAA TAC ACC ACC CAA TAC TAC AGC CTT GAT GCC CAA ATA ACA Asn Asp Lys Tyr Thr Thr Gln Tyr Tyr Ser Leu Asp Ala Gln Ile Thr 275 280 285	864
GGC AAC CGC TTC AAC GGT AAG GCG ATA CGG ACC GAC AAA CCC GAC ACT Gly Asn Arg Phe Asn Gly Lys Ala Ile Arg Thr Asp Lys Pro Asp Thr 290 295 300	912
GGA GGA ACC AAA CTA CAT CCC TTT GTT TCC GAC TCG TCT TCT TTG AGC Gly Gly Thr Lys Leu His Pro Phe Val Ser Asp Ser Ser Ser Leu Ser 305 310 315 320	960
GGC GGC TTT TTC GGT CCG AAG GGT GAG GAA TTG GGT TTC CGC TTT TTG Gly Gly Phe Phe Gly Pro Lys Gly Glu Glu Leu Gly Phe Arg Phe Leu 325 330 335	1008
AGC GAC GAT AAA AAA GTT GCG GTT GTC GGC AGC GCG AAA ACC AAA GAC Ser Asp Asp Lys Lys Val Ala Val Val Gly Ser Ala Lys Thr Lys Asp 340 345 350	1056
AAA ACG GAA AAT GGC GCG GTG GCT TCA GGC GGC ACA GAT GCG GCA GCA Lys Thr Glu Asn Gly Ala Val Ala Ser Gly Gly Thr Asp Ala Ala Ala 355 360 365	1104
TCA AAC GGT GCG GCA GGC ACG TCG TCT GAA AAC AGT AAG CTG ACC ACG Ser Asn Gly Ala Ala Gly Thr Ser Ser Glu Asn Ser Lys Leu Thr Thr 370 375 380	1152
GTT TTG GAT GCG GTC GAG CTG AAA TTG GGC GAT AAG GAA GTC CAA AAG Val Leu Asp Ala Val Glu Leu Lys Leu Gly Asp Lys Glu Val Gln Lys 385 390 395 400	1200
CTC GAC AAC TTC AGC AAC GCC GCC CAA CTG GTT GTC GAC GGC ATT ATG Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu Val Val Asp Gly Ile Met 405 410 415	1248

ATT CCG CTC TTG CCC GAG GCT TCC GAA AGT GGG AAC AAT CAA GCC AAT Ile Pro Leu Leu Pro Glu Ala Ser Glu Ser Gly Asn Asn Gln Ala Asn 420 425 430	1296
CAA GGT ACA AAT GGC GGA ACA GCC TTT ACC CGC AAA TTT GAC CAC ACG Gln Gly Thr Asn Gly Gly Thr Ala Phe Thr Arg Lys Phe Asp His Thr 435 440 445	1344
CCG GAA AGT GAT AAA AAA GAC GCC CAA GCA GGT ACG CAG ACG AAT GGG Pro Glu Ser Asp Lys Lys Asp Ala Gln Ala Gly Thr Gln Thr Asn Gly 450 455 460	1392
GCG CAA ACC GCT TCA AAT ACG GCA GGT GAT ACC AAT GGC AAA ACA AAA Ala Gln Thr Ala Ser Asn Thr Ala Gly Asp Thr Asn Gly Lys Thr Lys 465 470 475 480	1440
ACC TAT GAA GTC GAA GTC TGC TGT TCC AAC CTC AAT TAT CTG AAA TAC Thr Tyr Glu Val Glu Val Cys Cys Ser Asn Leu Asn Tyr Leu Lys Tyr 485 490 495	1488
GGA ATG TTG ACG CGC AAA AAC AGC AAG TCC GCG ATG CAG GCA GGA GAA Gly Met Leu Thr Arg Lys Asn Ser Lys Ser Ala Met Gln Ala Gly Glu 500 505 510	1536
AGC AGT AGT CAA GCT GAT GCT AAA ACG GAA CAA GTT GAA CAA AGT ATG Ser Ser Ser Gln Ala Asp Ala Lys Thr Glu Gln Val Glu Gln Ser Met 515 520 525	1584
TTC CTC CAA GGC GAG CGC ACC GAT GAA AAA GAG ATT CCA AGC GAG CAA Phe Leu Gln Gly Glu Arg Thr Asp Glu Lys Glu Ile Pro Ser Glu Gln 530 535 540	1632
AAC ATC GTT TAT CGG GGG TCT TGG TAC GGA TAT ATT GCC AAC GAC AAA Asn Ile Val Tyr Arg Gly Ser Trp Tyr Gly Tyr Ile Ala Asn Asp Lys 545 550 555 560	1680
AGC ACA AGC TGG AGC GGC AAT GCT TCC AAT GCA ACG AGT GGC AAC AGG Ser Thr Ser Trp Ser Gly Asn Ala Ser Asn Ala Thr Ser Gly Asn Arg 565 570 575	1728
GCG GAA TTT ACT GTG AAT TTT GCC GAT AAA AAA ATT ACT GGT ACG TTA Ala Glu Phe Thr Val Asn Phe Ala Asp Lys Lys Ile Thr Gly Thr Leu 580 585 590	1776
ACC GCT GAC AAC AGG CAG GAG GCA ACC TTT ACC ATT GAT GGT AAT ATT Thr Ala Asp Asn Arg Gln Glu Ala Thr Phe Thr Ile Asp Gly Asn Ile 595 600 605	1824
AAG GAC AAC GGC TTT GAA GGT ACG GCG AAA ACT GCT GAG TCA GGT TTT Lys Asp Asn Gly Phe Glu Gly Thr Ala Lys Thr Ala Glu Ser Gly Phe 610 615 620	1872
GAT CTC GAT CAA AGC AAT ACC ACC CGC ACG CCT AAG GCA TAT ATC ACA Asp Leu Asp Gln Ser Asn Thr Thr Arg Thr Pro Lys Ala Tyr Ile Thr 625 630 635 640	1920
GAT GCC AAG GTG CAG GGC GGT TTT TAC GGG CCC AAA GCC GAA GAG TTG Asp Ala Lys Val Gln Gly Gly Phe Tyr Gly Pro Lys Ala Glu Glu Leu 645 650 655	1968
GGC GGA TGG TTT GCC TAT CCG GGC GAT AAA CAA ACG AAA AAT GCA ACA Gly Gly Trp Phe Ala Tyr Pro Gly Asp Lys Gln Thr Lys Asn Ala Thr 660 665 670	2016

AAT GCA TCC GGC AAT AGC AGT GCA ACT GTC GTA TTC GGT GCG AAA CGC 2064
 Asn Ala Ser Gly Asn Ser Ser Ala Thr Val Val Phe Gly Ala Lys Arg
 675 680 685

CAA CAG CCT GTG CGA TAACGCAAGC CCAAAAAGAC CAAGGCCGAT ACGGT 2114
 Gln Gln Pro Val Arg
 690

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 693 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Cys Leu Gly Gly Gly Gly Thr Phe Asp Leu Asp Ser Val Asp Thr Glu
 1 5 10 15

Ala Pro Arg Pro Asp Pro Lys Tyr Gln Asp Val Ser Ser Glu Lys Pro
 20 25 30

Gln Ala Gln Lys Asp Gln Gly Gly Tyr Gly Phe Ala Met Arg Leu Lys
 35 40 45

Arg Arg Asn Trp Tyr Ser Ala Ala Lys Glu Asp Glu Val Lys Leu Asn
 50 55 60

Glu Ser Asp Trp Glu Thr Thr Gly Leu Pro Thr Glu Pro Lys Lys Leu
 65 70 75 80

Pro Leu Lys Gln Glu Ser Val Ile Ser Lys Val Gln Ala Asn Asn Gly
 85 90 95

Asp Asn Asn Ile Tyr Thr Ser Pro Tyr Leu Thr Gln Ser Asn His Gln
 100 105 110

Asn Ser Ser Ile Asn Gly Gly Ala Asn Leu Pro Lys Asn Glu Val Thr
 115 120 125

Asn Tyr Lys Asp Phe Lys Tyr Val Tyr Ser Gly Trp Phe Tyr Lys His
 130 135 140

Ala Lys Asn Glu Ile Ile Arg Glu Asn Ser Ser Ile Lys Gly Ala Lys
 145 150 155 160

Asn Gly Asp Asp Gly Tyr Ile Phe Tyr His Gly Lys Glu Pro Ser Arg
 165 170 175

Gln Leu Pro Ala Ser Gly Thr Val Thr Tyr Lys Gly Val Trp His Phe
 180 185 190

Ala Thr Asp Val Lys Lys Ser Gln Asn Phe Arg Asp Ile Ile Gln Pro
 195 200 205

Ser Lys Lys Gln Gly Asp Arg Tyr Ser Gly Phe Ser Gly Asp Asp Asp
 210 215 220

Glu Gln Tyr Ser Asn Lys Asn Glu Ser Met Leu Lys Asp Gly Gln Glu
 225 230 235 240

Gly Tyr Gly Phe Thr Ser Asn Leu Glu Val Asp Phe Gly Ser Lys Lys
245 250 255
Leu Thr Gly Lys Leu Ile Arg Asn Asn Arg Val Thr Asn Ala Pro Thr
260 265 270
Asn Asp Lys Tyr Thr Thr Gln Tyr Tyr Ser Leu Asp Ala Gln Ile Thr
275 280 285
Gly Asn Arg Phe Asn Gly Lys Ala Ile Arg Thr Asp Lys Pro Asp Thr
290 295 300
Gly Gly Thr Lys Leu His Pro Phe Val Ser Asp Ser Ser Ser Leu Ser
305 310 315 320
Gly Gly Phe Phe Gly Pro Lys Gly Glu Glu Leu Gly Phe Arg Phe Leu
325 330 335
Ser Asp Asp Lys Lys Val Ala Val Val Gly Ser Ala Lys Thr Lys Asp
340 345 350
Lys Thr Glu Asn Gly Ala Val Ala Ser Gly Gly Thr Asp Ala Ala Ala
355 360 365
Ser Asn Gly Ala Ala Gly Thr Ser Ser Glu Asn Ser Lys Leu Thr Thr
370 375 380
Val Leu Asp Ala Val Glu Leu Lys Leu Gly Asp Lys Glu Val Gln Lys
385 390 395 400
Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu Val Val Asp Gly Ile Met
405 410 415
Ile Pro Leu Leu Pro Glu Ala Ser Glu Ser Gly Asn Asn Gln Ala Asn
420 425 430
Gln Gly Thr Asn Gly Gly Thr Ala Phe Thr Arg Lys Phe Asp His Thr
435 440 445
Pro Glu Ser Asp Lys Lys Asp Ala Gln Ala Gly Thr Gln Thr Asn Gly
450 455 460
Ala Gln Thr Ala Ser Asn Thr Ala Gly Asp Thr Asn Gly Lys Thr Lys
465 470 475 480
Thr Tyr Glu Val Glu Val Cys Cys Ser Asn Leu Asn Tyr Leu Lys Tyr
485 490 495
Gly Met Leu Thr Arg Lys Asn Ser Lys Ser Ala Met Gln Ala Gly Glu
500 505 510
Ser Ser Ser Gln Ala Asp Ala Lys Thr Glu Gln Val Glu Gln Ser Met
515 520 525
Phe Leu Gln Gly Glu Arg Thr Asp Glu Lys Glu Ile Pro Ser Glu Gln
530 535 540
Asn Ile Val Tyr Arg Gly Ser Trp Tyr Gly Tyr Ile Ala Asn Asp Lys
545 550 555 560
Ser Thr Ser Trp Ser Gly Asn Ala Ser Asn Ala Thr Ser Gly Asn Arg
565 570 575

Ala Glu Phe Thr Val Asn Phe Ala Asp Lys Lys Ile Thr Gly Thr Leu
 580 585 590

Thr Ala Asp Asn Arg Gln Glu Ala Thr Phe Thr Ile Asp Gly Asn Ile
 595 600 605

Lys Asp Asn Gly Phe Glu Gly Thr Ala Lys Thr Ala Glu Ser Gly Phe
 610 615 620

Asp Leu Asp Gln Ser Asn Thr Thr Arg Thr Pro Lys Ala Tyr Ile Thr
 625 630 635 640

Asp Ala Lys Val Gln Gly Gly Phe Tyr Gly Pro Lys Ala Glu Glu Leu
 645 650 655

Gly Gly Trp Phe Ala Tyr Pro Gly Asp Lys Gln Thr Lys Asn Ala Thr
 660 665 670

Asn Ala Ser Gly Asn Ser Ser Ala Thr Val Val Phe Gly Ala Lys Arg
 675 680 685

Gln Gln Pro Val Arg
 690

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2114 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: N. meningitidis
 (B) STRAIN: S3032

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
 (B) LOCATION: 1..2097

(ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) LOCATION: 1..2097

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

TGT TTG GGC GGA GGC GGC GGC AGT TTC GAT CTT GAT TCT GTC GAT ACC	48
Cys Leu Gly Gly Gly Gly Gly Ser Phe Asp Leu Asp Ser Val Asp Thr	
1 5 10 15	
GAA GCC CCG CGT CCC GCG CCA AAG TAT CAA GAT GTT TCT TCC GAA AAA	96
Glu Ala Pro Arg Pro Ala Pro Lys Tyr Gln Asp Val Ser Ser Glu Lys	
20 25 30	
CCG CAA GCC CAA AAA GAC CAA GGC GGA TAC GGT TTT GCG ATG AGG TTG	144
Pro Gln Ala Gln Lys Asp Gln Gly Tyr Gly Phe Ala Met Arg Leu	
35 40 45	
AAA CGG AGG AAT TGG TAT CCG TCG GCA AAA GAA AAC GAG GTT AAA CTG	192
Lys Arg Arg Asn Trp Tyr Pro Ser Ala Lys Glu Asn Glu Val Lys Leu	
50 55 60	

AAT GAG AGT GAT TGG GAG ACG ACA GGA TTG CCA AGC AAT CCC AAA AAC 240
Asn Glu Ser Asp Trp Glu Thr Thr Gly Leu Pro Ser Asn Pro Lys Asn 80
65 70 75

TTA CCT GAG CGA CAG AAA TCG GTT ATT GAT CAA GTA GAA ACA GAT GGC 288
Leu Pro Glu Arg Gln Lys Ser Val Ile Asp Gln Val Glu Thr Asp Gly 95
85 90

GAC AGC AAT AAC AGC AAT ATT TAT TCT TCC CCC TAT CTC ACG CAA TCA 336
Asp Ser Asn Asn Ser Asn Ile Tyr Ser Ser Pro Tyr Leu Thr Gln Ser 110
100 105

AAC CAT CAA AAC GGC AAC ACT GGC AAC GGT GTA AAC CAA CCA AAA AAC 384
Asn His Gln Asn Gly Asn Thr Gly Asn Gly Val Asn Gln Pro Lys Asn 125
115 120

GAA GTA ACA GAT TAC AAA AAT TTT AAA TAT GTT TAT TCC GGC TGG TTT 432
Glu Val Thr Asp Tyr Lys Asn Phe Lys Tyr Val Tyr Ser Gly Trp Phe 140
130 135

TAC AAA CAC GCC AAA CGA GAG GTT AAC TTA GCG GTG GAA CCT AAA ATT 480
Tyr Lys His Ala Lys Arg Glu Val Asn Leu Ala Val Glu Pro Lys Ile 160
145 150 155

GCA AAA AAC GGC GAC GAC GGT TAT ATC TTC TAT CAC GGT AAA GAC CCT 528
Ala Lys Asn Gly Asp Asp Gly Tyr Ile Phe Tyr His Gly Lys Asp Pro 175
165 170

TCC CGA CAA CTT CCC GCT TCT GGA AAA ATT ACC TAT AAA GGT GTG TGG 576
Ser Arg Gln Leu Pro Ala Ser Gly Lys Ile Thr Tyr Lys Gly Val Trp 190
180 185

CAT TTT GCG ACC GAT ACA AAA AGG GGT CAA AAA TTT CGT GAA ATT ATC 624
His Phe Ala Thr Asp Thr Lys Arg Gly Gln Lys Phe Arg Glu Ile Ile 205
195 200

CAA CCT TCA AAA AAT CAA GGC GAC AGA TAT AGC GGA TTT TCG GGT GAT 672
Gln Pro Ser Lys Asn Gln Gly Asp Arg Tyr Ser Gly Phe Ser Gly Asp 220
210 215

GAT GAT GAA CAA TAT TCT AAT AAA AAC GAA TCC ATG CTG AAA GAT GGT 720
Asp Asp Glu Gln Tyr Ser Asn Lys Asn Glu Ser Met Leu Lys Asp Gly 240
225 230 235

CAT GAA GGT TAT GGT TTT GCC TCG AAT TTA GAA GTG GAT TTC GAC AAT 768
His Glu Gly Tyr Gly Phe Ala Ser Asn Leu Glu Val Asp Phe Asp Asn 255
245 250

AAA AAA TTG ACG GGT AAA TTA ATA CGC AAT AAT GCG AAC CAA AAT AAT 816
Lys Lys Leu Thr Gly Lys Leu Ile Arg Asn Asn Ala Asn Gln Asn Asn 270
260 265

AAT ACT AAT AAT GAC AAA CAC ACC ACC CAA TAC TAC AGC CTT GAT GCG 864
Asn Thr Asn Asn Asp Lys His Thr Thr Gln Tyr Tyr Ser Leu Asp Ala 285
275 280

ACG CTT AAG GGA AAC CGC TTC AGC GGA AAA GCG GAA GCA ACC GAC AAA 912
Thr Leu Lys Gly Asn Arg Phe Ser Gly Lys Ala Glu Ala Thr Asp Lys 300
290 295

CCC AAA AAC GAC GGC GAA ACC AAG GAA CAT CCC TTT GTT TCC GAC TCG 960
Pro Lys Asn Asp Gly Glu Thr Lys Glu His Pro Phe Val Ser Asp Ser 320
305 310 315

TCT TCT TTG AGC GGC GGC TTT TTC GGC CCG CAG GGT GAG GAA TTG GGT Ser Ser Leu Ser Gly Gly Phe Phe Gly Pro Gln Gly Glu Glu Leu Gly 325 330 335	1008
TTC CGC TTT TTG AGC AAC GAT CAA AAA GTT GCC GTT GTC GGC AGC GCG Phe Arg Phe Leu Ser Asn Asp Gln Lys Val Ala Val Val Gly Ser Ala 340 345 350	1056
AAA ACC AAA GAC AAA CCC GCA AAT GGC AAT ACT GCG GAG GCT TCA GGC Lys Thr Lys Asp Lys Pro Ala Asn Gly Asn Thr Ala Glu Ala Ser Gly 355 360 365	1104
GGC ACA GAT GCG GCA GCA TCG GGC GGT GCG GCA GGC ACG TCG TCT GAA Gly Thr Asp Ala Ala Ser Gly Gly Ala Ala Gly Thr Ser Ser Glu 370 375 380	1152
AAC AGT AAG CTG ACC ACC GTT TTG GAT GCG GTC GAG CTG ACG CAC GGC Asn Ser Lys Leu Thr Thr Val Leu Asp Ala Val Glu Leu Thr His Gly 385 390 395 400	1200
GGC ACA GCA ATC AAA AAT CTC GAC AAC TTC AGC AAT GCC GCC CAA CTG Gly Thr Ala Ile Lys Asn Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu 405 410 415	1248
GTT GTC GAC GGC ATT ATG ATT CCG CTC CTG CCT CAA AAT TCA ACA GGC Val Val Asp Gly Ile Met Ile Pro Leu Leu Pro Gln Asn Ser Thr Gly 420 425 430	1296
AAA AAT AAT CAG CCC GAT CAA GGT AAA AAC GGC GGA ACA GCC TTT ATC Lys Asn Asn Gln Pro Asp Gln Gly Lys Asn Gly Gly Thr Ala Phe Ile 435 440 445	1344
TAT AAA ACG ACC TAC ACG CCG AAA AAC GAT GAC AAA GAT ACC AAA GCC Tyr Lys Thr Thr Tyr Thr Pro Lys Asn Asp Asp Lys Asp Thr Lys Ala 450 455 460	1392
CAA ACA GTC ACG GGC GGC ACG CAA ACC GCT TCA AAT ACG GCA GGT GAT Gln Thr Val Thr Gly Gly Thr Gln Thr Ala Ser Asn Thr Ala Gly Asp 465 470 475 480	1440
GCC AAT GGC AAA ACA AAA ACC TAT GAA GTC GAA GTC TGC TGT TCC AAC Ala Asn Gly Lys Thr Lys Thr Tyr Glu Val Glu Val Cys Cys Ser Asn 485 490 495	1488
CTC AAT TAT CTG AAA TAC GGG TTG CTG ACG CGC AAA ACT GCC GGC AAC Leu Asn Tyr Leu Lys Tyr Gly Leu Leu Thr Arg Lys Thr Ala Gly Asn 500 505 510	1536
ACG GTG GGA AGC GGC AAC AGC AGC CCA ACC GCC GCC GCC CAA ACG GAC Thr Val Gly Ser Gly Asn Ser Ser Pro Thr Ala Ala Ala Gln Thr Asp 515 520 525	1584
GCG CAG AGT ATG TTC CTC CAA GGC GAG CGC ACC GAT GAA AAC AAG ATT Ala Gln Ser Met Phe Leu Gln Gly Glu Arg Thr Asp Glu Asn Lys Ile 530 535 540	1632
CCA AGC GAG CAA AAC GTC GTT TAT CGG GGG TCT TGG TAC GGG CAT ATT Pro Ser Glu Gln Asn Val Val Tyr Arg Gly Ser Trp Tyr Gly His Ile 545 550 555 560	1680
GCC AGC AGC ACA AGC TGG AGC GGC AAT GCT TCT GAT AAA GAG GGC GGC Ala Ser Ser Thr Ser Trp Ser Gly Asn Ala Ser Asp Lys Glu Gly Gly 565 570 575	1728

AAC AGG GCG GAA TTT ACT GTG AAT TTT GGC GAG AAA AAA ATT ACC GGC 1776
 Asn Arg Ala Glu Phe Thr Val Asn Phe Gly Glu Lys Lys Ile Thr Gly
 580 585 590
 ACG TTA ACC GCT GAA AAC AGG CAG GAG GCA ACC TTT ACC ATT GAT GGT 1824
 Thr Leu Thr Ala Glu Asn Arg Gln Glu Ala Thr Phe Thr Ile Asp Gly
 595 600 605
 AAG ATT GAG GGC AAC GGT TTT TCC GGT ACG GCA AAA ACT GCT GAA TTA 1872
 Lys Ile Glu Gly Asn Gly Phe Ser Gly Thr Ala Lys Thr Ala Glu Leu
 610 615 620
 GGT TTT GAT CTC GAT CAA AAA AAT ACC ACC CGC ACG CCT AAG GCA TAT 1920
 Gly Phe Asp Leu Asp Gln Lys Asn Thr Thr Arg Thr Pro Lys Ala Tyr
 625 630 635 640
 ATC ACA GAT GCC AAG GTA AAG GGC GGT TTT TAC GGG CCC AAA GCC GAA 1968
 Ile Thr Asp Ala Lys Val Lys Gly Gly Phe Tyr Gly Pro Lys Ala Glu
 645 650 655
 GAG TTG GGC GGA TGG TTT GCC TAT TCG GAC GAT AAA CAA ACG AAA AAT 2016
 Glu Leu Gly Gly Trp Phe Ala Tyr Ser Asp Asp Lys Gln Thr Lys Asn
 660 665 670
 GCA ACA GAT GCA TCC GGC AAT GGA AAT TCA GCA AGC AGT GCA ACT GTC 2064
 Ala Thr Asp Ala Ser Gly Asn Gly Asn Ser Ala Ser Ser Ala Thr Val
 675 680 685
 GTA TTC GGT GCG AAA CGC CAA CAG CCG GTG CAA TAAACCAAGG CCGATAC 2114
 Val Phe Gly Ala Lys Arg Gln Gln Pro Val Gln
 690 695

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 699 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Cys Leu Gly Gly Gly Gly Gly Ser Phe Asp Leu Asp Ser Val Asp Thr
 1 5 10 15
 Glu Ala Pro Arg Pro Ala Pro Lys Tyr Gln Asp Val Ser Ser Glu Lys
 20 25 30
 Pro Gln Ala Gln Lys Asp Gln Gly Gly Tyr Gly Phe Ala Met Arg Leu
 35 40 45
 Lys Arg Arg Asn Trp Tyr Pro Ser Ala Lys Glu Asn Glu Val Lys Leu
 50 55 60
 Asn Glu Ser Asp Trp Glu Thr Thr Gly Leu Pro Ser Asn Pro Lys Asn
 65 70 75 80
 Leu Pro Glu Arg Gln Lys Ser Val Ile Asp Gln Val Glu Thr Asp Gly
 85 90 95

Asp Ser Asn Asn Ser Asn Ile Tyr Ser Ser Pro Tyr Leu Thr Gln Ser
 100 105 110
 Asn His Gln Asn Gly Asn Thr Gly Asn Gly Val Asn Gln Pro Lys Asn
 115 120 125
 Glu Val Thr Asp Tyr Lys Asn Phe Lys Tyr Val Tyr Ser Gly Trp Phe
 130 135 140
 Tyr Lys His Ala Lys Arg Glu Val Asn Leu Ala Val Glu Pro Lys Ile
 145 150 155 160
 Ala Lys Asn Gly Asp Asp Gly Tyr Ile Phe Tyr His Gly Lys Asp Pro
 165 170 175
 Ser Arg Gln Leu Pro Ala Ser Gly Lys Ile Thr Tyr Lys Gly Val Trp
 180 185 190
 His Phe Ala Thr Asp Thr Lys Arg Gly Gln Lys Phe Arg Glu Ile Ile
 195 200 205
 Gln Pro Ser Lys Asn Gln Gly Asp Arg Tyr Ser Gly Phe Ser Gly Asp
 210 215 220
 Asp Asp Glu Gln Tyr Ser Asn Lys Asn Glu Ser Met Leu Lys Asp Gly
 225 230 235 240
 His Glu Gly Tyr Gly Phe Ala Ser Asn Leu Glu Val Asp Phe Asp Asn
 245 250 255
 Lys Lys Leu Thr Gly Lys Leu Ile Arg Asn Asn Ala Asn Gln Asn Asn
 260 265 270
 Asn Thr Asn Asn Asp Lys His Thr Thr Gln Tyr Tyr Ser Leu Asp Ala
 275 280 285
 Thr Leu Lys Gly Asn Arg Phe Ser Gly Lys Ala Glu Ala Thr Asp Lys
 290 295 300
 Pro Lys Asn Asp Gly Glu Thr Lys Glu His Pro Phe Val Ser Asp Ser
 305 310 315 320
 Ser Ser Leu Ser Gly Gly Phe Phe Gly Pro Gln Gly Glu Glu Leu Gly
 325 330 335
 Phe Arg Phe Leu Ser Asn Asp Gln Lys Val Ala Val Val Gly Ser Ala
 340 345 350
 Lys Thr Lys Asp Lys Pro Ala Asn Gly Asn Thr Ala Glu Ala Ser Gly
 355 360 365
 Gly Thr Asp Ala Ala Ala Ser Gly Gly Ala Ala Gly Thr Ser Ser Glu
 370 375 380
 Asn Ser Lys Leu Thr Thr Val Leu Asp Ala Val Glu Leu Thr His Gly
 385 390 395 400
 Gly Thr Ala Ile Lys Asn Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu
 405 410 415
 Val Val Asp Gly Ile Met Ile Pro Leu Leu Pro Gln Asn Ser Thr Gly
 420 425 430

Lys Asn Asn Gln Pro Asp Gln Gly Lys Asn Gly Gly Thr Ala Phe Ile
435 440 445
Tyr Lys Thr Thr Tyr Thr Pro Lys Asn Asp Asp Lys Asp Thr Lys Ala
450 455 460
Gln Thr Val Thr Gly Gly Thr Gln Thr Ala Ser Asn Thr Ala Gly Asp
465 470 475 480
Ala Asn Gly Lys Thr Lys Thr Tyr Glu Val Glu Val Cys Cys Ser Asn
485 490 495
Leu Asn Tyr Leu Lys Tyr Gly Leu Leu Thr Arg Lys Thr Ala Gly Asn
500 505 510
Thr Val Gly Ser Gly Asn Ser Ser Pro Thr Ala Ala Ala Gln Thr Asp
515 520 525
Ala Gln Ser Met Phe Leu Gln Gly Glu Arg Thr Asp Glu Asn Lys Ile
530 535 540
Pro Ser Glu Gln Asn Val Val Tyr Arg Gly Ser Trp Tyr Gly His Ile
545 550 555 560
Ala Ser Ser Thr Ser Trp Ser Gly Asn Ala Ser Asp Lys Glu Gly Gly
565 570 575
Asn Arg Ala Glu Phe Thr Val Asn Phe Gly Glu Lys Lys Ile Thr Gly
580 585 590
Thr Leu Thr Ala Glu Asn Arg Gln Glu Ala Thr Phe Thr Ile Asp Gly
595 600 605
Lys Ile Glu Gly Asn Gly Phe Ser Gly Thr Ala Lys Thr Ala Glu Leu
610 615 620
Gly Phe Asp Leu Asp Gln Lys Asn Thr Thr Arg Thr Pro Lys Ala Tyr
625 630 635 640
Ile Thr Asp Ala Lys Val Lys Gly Gly Phe Tyr Gly Pro Lys Ala Glu
645 650 655
Glu Leu Gly Gly Trp Phe Ala Tyr Ser Asp Asp Lys Gln Thr Lys Asn
660 665 670
Ala Thr Asp Ala Ser Gly Asn Gly Asn Ser Ala Ser Ser Ala Thr Val
675 680 685
Val Phe Gly Ala Lys Arg Gln Gln Pro Val Gln
690 695

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 198 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: N. meningitidis
(B) STRAIN: IM2169

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

Thr Lys Asp Lys Leu Glu Asn Gly Ala Ala Ala Ser Gly Ser Thr Gly
 1 5 10 15
 Ala Ala Ala Ser Gly Gly Ala Ala Gly Thr Ser Ser Glu Asn Ser Lys
 20 25 30
 Leu Thr Thr Val Leu Asp Ala Val Glu Leu Thr Leu Asn Asp Lys Lys
 35 40 45
 Ile Lys Asn Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu Val Val Asp
 50 55 60
 Gly Ile Met Ile Pro Leu Leu Pro Lys Asp Ser Glu Ser Gly Asn Thr
 65 70 75 80
 Gln Ala Asp Lys Gly Lys Asn Gly Gly Thr Glu Phe Thr Arg Lys Phe
 85 90 95
 Glu His Thr Pro Glu Ser Asp Lys Lys Asp Ala Gln Ala Gly Thr Gln
 100 105 110
 Thr Asn Gly Ala Gln Thr Ala Ser Asn Thr Ala Gly Asp Thr Asn Gly
 115 120 125
 Lys Thr Lys Thr Tyr Glu Val Glu Val Cys Cys Ser Asn Leu Asn Tyr
 130 135 140
 Leu Lys Tyr Gly Met Leu Thr Arg Lys Asn Ser Lys Ser Ala Met Gln
 145 150 155 160
 Ala Gly Gly Asn Ser Ser Gln Ala Asp Ala Lys Thr Glu Gln Val Glu
 165 170 175
 Gln Ser Met Phe Leu Gln Gly Glu Arg Thr Asp Glu Lys Glu Ile Pro
 180 185 190
 Thr Asp Gln Asn Val Val
 195

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 198 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: N. meningitidis
 (B) STRAIN: 6940

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

Thr Lys Asp Lys Thr Glu Asn Gly Ala Val Ala Ser Gly Gly Thr Asp
 1 5 10 15
 Ala Ala Ala Ser Asn Gly Ala Ala Gly Thr Ser Ser Glu Asn Ser Lys
 20 25 30

Leu Thr Thr Val Leu Asp Ala Val Glu Leu Lys Leu Gly Asp Lys Glu
 35 40 45
 Val Gln Lys Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu Val Val Asp
 50 55 60
 Gly Ile Met Ile Pro Leu Leu Pro Glu Ala Ser Glu Ser Gly Asn Asn
 65 70 75 80
 Gln Ala Asn Gln Gly Thr Asn Gly Gly Thr Ala Phe Thr Arg Lys Phe
 85 90 95
 Asp His Thr Pro Glu Ser Asp Lys Lys Asp Ala Gln Ala Gly Thr Gln
 100 105 110
 Thr Asn Gly Ala Gln Thr Ala Ser Asn Thr Ala Gly Asp Thr Asn Gly
 115 120 125
 Lys Thr Lys Thr Tyr Glu Val Glu Val Cys Cys Ser Asn Leu Asn Tyr
 130 135 140
 Leu Lys Tyr Gly Met Leu Thr Arg Lys Asn Ser Lys Ser Ala Met Gln
 145 150 155 160
 Ala Gly Glu Ser Ser Ser Gln Ala Asp Ala Lys Thr Glu Gln Val Glu
 165 170 175
 Gln Ser Met Phe Leu Gln Gly Glu Arg Thr Asp Glu Lys Glu Ile Pro
 180 185 190
 Ser Glu Gln Asn Ile Val
 195

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 198 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: N. meningitidis
 (B) STRAIN: 2223

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

Thr Lys Asp Lys Thr Glu Asn Gly Ala Val Ala Ser Gly Gly Thr Asp
 1 5 10
 Ala Ala Ala Ser Asn Gly Ala Ala Gly Thr Ser Ser Glu Asn Ser Lys
 20 25 30
 Leu Thr Thr Val Leu Asp Ala Val Glu Leu Lys Leu Gly Asp Lys Glu
 35 40 45
 Val Gln Lys Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu Val Val Asp
 50 55 60
 Gly Ile Met Ile Pro Leu Leu Pro Glu Ala Ser Glu Ser Gly Asn Asn
 65 70 75 80

Gln Ala Asn Gln Gly Thr Asn Gly Gly Thr Ala Phe Thr Arg Lys Phe
 85 90 95
 Asp His Thr Pro Glu Ser Asp Lys Lys Asp Ala Gln Ala Gly Thr Gln
 100 105 110
 Ala Asn Gly Ala Gln Thr Ala Ser Asn Thr Ala Gly Asp Thr Asn Gly
 115 120 125
 Lys Thr Lys Thr Tyr Glu Val Glu Val Cys Cys Ser Asn Leu Asn Tyr
 130 135 140
 Leu Lys Tyr Gly Met Leu Thr Arg Lys Asn Ser Lys Ser Ala Met Gln
 145 150 155 160
 Ala Gly Glu Ser Ser Ser Gln Ala Asp Ala Lys Thr Glu Gln Val Gly
 165 170 175
 Gln Ser Met Phe Leu Gln Gly Glu Arg Thr Asp Glu Lys Glu Ile Pro
 180 185 190
 Ser Glu Gln Asn Ile Val
 195

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 198 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: N. meningitidis
 (B) STRAIN: C708

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

Thr Gln Asp Lys Pro Arg Asn Gly Ala Val Ala Ser Gly Gly Thr Gly
 1 5 10 15
 Ala Ala Arg Ser Asn Gly Ala Ala Gly Gln Ser Ser Glu Asn Ser Lys
 20 25 30
 Leu Thr Thr Val Leu Asp Ala Val Glu Leu Thr Leu Asn Asp Lys Lys
 35 40 45
 Ile Lys Asn Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu Val Val Asp
 50 55 60
 Gly Ile Met Ile Pro Leu Leu Pro Glu Ala Ser Glu Ser Gly Lys Asn
 65 70 75 80
 Gln Ala Asn Gln Gly Thr Asn Gly Gly Thr Ala Phe Thr Arg Lys Phe
 85 90 95
 Asn His Thr Pro Lys Ser Asp Glu Lys Asp Thr Gln Ala Gly Thr Ala
 100 105 110
 Glu Asn Gly Asn Pro Ala Ala Ser Asn Thr Ala Gly Asp Ala Asn Gly
 115 120 125

Lys Thr Lys Thr Tyr Glu Val Glu Val Cys Cys Ser Asn Leu Asn Tyr
 130 135 140
 Leu Lys Tyr Gly Met Leu Thr Arg Lys Asn Ser Lys Ser Ala Met Gln
 145 150 155 160
 Ala Gly Glu Ser Ser Ser Gln Ala Asp Ala Lys Thr Glu Gln Val Gly
 165 170 175
 Gln Ser Met Phe Leu Gln Gly Glu Arg Thr Asp Glu Lys Glu Ile Pro
 180 185 190
 Asn Asp Gln Asn Val Val
 195

(2) INFORMATION FOR SEQ ID NO: 15:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 211 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: N. meningitidis
 (B) STRAIN: M978

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

Thr Gln Asp Lys Ala Ala Asn Gly Asn Thr Ala Ala Ala Ser Gly Gly
 1 5 10 15
 Thr Asp Ala Ala Ala Ser Asn Gly Ala Ala Gly Thr Ser Ser Glu Asn
 20 25 30
 Ser Lys Leu Thr Thr Val Leu Asp Ala Val Glu Leu Thr Leu Asn Asp
 35 40 45
 Lys Lys Ile Lys Asn Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu Val
 50 55 60
 Val Asp Gly Ile Met Ile Pro Leu Leu Pro Glu Thr Ser Glu Ser Gly
 65 70 75 80
 Ser Asn Gln Ala Asp Lys Gly Lys Lys Gly Lys Asn Gly Lys Asn Gly
 85 90 95
 Gly Thr Asp Phe Thr Tyr Lys Thr Thr Tyr Thr Pro Lys Asn Asp Asp
 100 105 110
 Lys Asp Thr Lys Ala Gln Thr Gly Ala Ala Gly Ser Ser Gly Ala Gln
 115 120 125
 Thr Asp Leu Gly Lys Ala Asp Val Asn Gly Gly Lys Ala Glu Thr Lys
 130 135 140
 Thr Tyr Glu Val Glu Val Cys Cys Ser Asn Leu Asn Tyr Leu Lys Tyr
 145 150 155 160
 Gly Met Leu Thr Arg Lys Asn Ser Lys Ser Ala Met Gln Ala Gly Gly
 165 170 175

Asn Ser Ser Gln Ala Asp Ala Lys Thr Glu Gln Val Glu Gln Ser Met
180 185 190

Phe Leu Gln Gly Glu Arg Thr Asp Glu Lys Glu Ile Pro Asn Asp Gln
195 200 205

Asn Val Val
210

(2) INFORMATION FOR SEQ ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 200 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *N. meningitidis*
(B) STRAIN: 1610

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

Lys Arg Asp Lys Ala Glu Ser Gly Gly Gly Asn Gly Ala Ser Gly Gly
1 5 10 15

Thr Asp Ala Ala Ala Ser Asn Gly Ala Ala Gly Thr Ser Ser Glu Asn
20 25 30

Ser Lys Leu Thr Thr Val Leu Asp Ala Val Glu Leu Lys Ser Gly Gly
35 40 45

Lys Glu Val Lys Asn Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu Val
50 55 60

Val Asp Gly Ile Met Ile Pro Leu Leu Pro Lys Asp Ser Glu Ser Gly
65 70 75 80

Asn Thr Gln Ala Asp Lys Gly Lys Asn Gly Gly Thr Lys Phe Thr Arg
85 90 95

Lys Phe Glu His Thr Pro Glu Ser Asp Lys Lys Asp Ala Gln Ala Gly
100 105 110

Thr Gln Thr Asn Gly Ala Gln Thr Ala Ser Asn Thr Ala Gly Asp Thr
115 120 125

Asn Gly Lys Thr Lys Thr Tyr Glu Val Glu Val Cys Cys Ser Asn Leu
130 135 140

Asn Tyr Leu Lys Tyr Gly Leu Leu Thr Arg Lys Thr Ala Gly Asn Thr
145 150 155 160

Gly Glu Gly Gly Asn Gly Ser Gln Thr Ala Ala Ala Gln Thr Ala Gln
165 170 175

Gly Ala Gln Ser Met Phe Leu Gln Gly Glu Arg Thr Asp Glu Lys Glu
180 185 190

Ile Pro Ser Glu Gln Asn Val Val
195 200

(2) INFORMATION FOR SEQ ID NO: 17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 200 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: N. meningitidis
(B) STRAIN: 867

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

Thr Lys Asp Lys Pro Arg Asn Gly Ala Val Ala Ser Gly Gly Thr Asp
1 5 10 15
Ala Ala Ala Ser Asn Gly Ala Ala Gly Thr Ser Ser Glu Asn Gly Lys
20 25 30
Leu Thr Thr Val Leu Asp Ala Val Glu Leu Thr Leu Asn Asp Lys Lys
35 40 45
Ile Lys Asn Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu Val Val Ser
50 55 60
Gly Ile Met Ile Pro Leu Met Pro Glu Thr Ser Glu Ser Gly Asn Asn
65 70 75 80
Gln Ala Asp Lys Gly Lys Asn Gly Gly Thr Ala Phe Thr Arg Lys Phe
85 90 95
Asp His Thr Pro Lys Ser Asp Glu Lys Asp Thr Gln Ala Gly Thr Pro
100 105 110
Thr Asn Gly Ala Gln Thr Ala Ser Gly Thr Ala Gly Val Thr Gly Gly
115 120 125
Gln Ala Gly Lys Thr Tyr Ala Val Glu Val Cys Cys Ser Asn Leu Asn
130 135 140
Tyr Leu Lys Tyr Gly Leu Leu Thr Arg Lys Thr Ala Asp Asn Thr Val
145 150 155 160
Gly Ser Gly Asn Gly Ser Ser Thr Ala Ala Ala Gln Thr Ala Gln Gly
165 170 175
Ala Gln Ser Met Phe Leu Gln Gly Glu Arg Thr Asp Glu Lys Glu Ile
180 185 190
Pro Lys Glu Gln Gln Asp Ile Val
195 200

(2) INFORMATION FOR SEQ ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 198 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: N. meningitidis
(B) STRAIN: S3032

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

Thr Lys Asp Lys Pro Ala Asn Gly Asn Thr Ala Glu Ala Ser Gly Gly
 1 5 10 15
 Thr Asp Ala Ala Ala Ser Gly Gly Ala Ala Gly Thr Ser Ser Glu Asn
 20 25 30
 Ser Lys Leu Thr Thr Val Leu Asp Ala Val Glu Leu Thr His Gly Gly
 35 40 45
 Thr Ala Ile Lys Asn Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu Val
 50 55 60
 Val Asp Gly Ile Met Ile Pro Leu Leu Pro Gln Asn Ser Thr Gly Lys
 65 70 75 80
 Asn Asn Gln Pro Asp Gln Gly Lys Asn Gly Gly Thr Ala Phe Ile Tyr
 85 90 95
 Lys Thr Thr Tyr Thr Pro Lys Asn Asp Asp Lys Asp Thr Lys Ala Gln
 100 105 110
 Thr Val Thr Gly Gly Thr Gln Thr Ala Ser Asn Thr Ala Gly Asp Ala
 115 120 125
 Asn Gly Lys Thr Lys Thr Tyr Glu Val Glu Val Cys Cys Ser Asn Leu
 130 135 140
 Asn Tyr Leu Lys Tyr Gly Leu Leu Thr Arg Lys Thr Ala Gly Asn Thr
 145 150 155 160
 Val Gly Ser Gly Asn Ser Ser Pro Thr Ala Ala Ala Gln Thr Asp Ala
 165 170 175
 Gln Ser Met Phe Leu Gln Gly Glu Arg Thr Asp Glu Asn Lys Ile Pro
 180 185 190
 Ser Glu Gln Asn Val Val
 195

(2) INFORMATION FOR SEQ ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 195 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: N. meningitidis
 (B) STRAIN: 891

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

Thr Lys Asp Lys Pro Gly Asn Gly Ala Arg Leu Gln Ala Ala Arg Cys
 1 5 10 15

Gly Thr Ser Asn Gly Ala Ala Gly Gln Ser Ser Glu Asn Ser Lys Leu
 20 25 30
 Thr Thr Val Leu Asp Ala Val Glu Leu Lys Leu Gly Asp Lys Glu Val
 35 40 45
 Gln Lys Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu Val Val Asp Gly
 50 55 60
 Ile Met Ile Pro Leu Leu Pro Lys Asp Ser Glu Ser Gly Lys Asn Gln
 65 70 75 80
 Ala Asp Lys Gly Lys Asn Gly Glu Thr Glu Phe Thr Arg Lys Phe Glu
 85 90 95
 His Thr Pro Glu Ser Asp Glu Lys Asp Ala Gln Ala Gly Thr Pro Ser
 100 105 110
 Asn Gly Ala Gln Thr Ala Ser Asn Thr Ala Gly Asp Thr Asn Gly Lys
 115 120 125
 Thr Lys Thr Tyr Glu Val Asn Leu Cys Ser Asn Leu Asn Tyr Leu Lys
 130 135 140
 Tyr Gly Leu Leu Thr Arg Lys Thr Ala Gly Asn Thr Gly Glu Gly Gly
 145 150 155 160
 Asn Ser Ser Pro Thr Ala Ala Gln Thr Ala Gln Gly Ala Gln Ser Met
 165 170 175
 Phe Leu Gln Gly Glu Arg Thr Asp Glu Lys Glu Ile Pro Asn Asp Gln
 180 185 190
 Asn Val Val
 195

(2) INFORMATION FOR SEQ ID NO: 20:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 29 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

AAACCCGGAT CCGTTGCCAG CGCTGCCGT

29

10 (2) INFORMATION FOR SEQ ID NO: 21:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 85 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

15

TTTTTTCATG AGATATCTGG CAACATTGTT GTTATCTCTG GCGGTGTTAA TCACCGCCGG 60
GTGCCTGGGT GCGGGCGGCA GTTTC 85

(2) INFORMATION FOR SEQ ID NO: 22:

- (1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

GTGTTTTTGT TGAGTGCATG CCTGGGTGGC 30

10 (2) INFORMATION FOR SEQ ID NO: 23:

- (1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 40 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

TGCGCAAGCT TACAGTTTGT CTTTGTTTTC CGCGCTGCCG 40

(2) INFORMATION FOR SEQ ID NO: 24:

- (1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 40 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

AAAAAGCATG CATAAAACT ACGCGTTACA CCATTCAAGC 40

(2) INFORMATION FOR SEQ ID NO: 25:

- (1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

TATATAAGCT TACGTTGCAG GCCCTGCCGC GTTTTCCCC 39

(2) INFORMATION FOR SEQ ID NO: 26:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

CCCGAATTCT GCCGTCTGAA GCCTTATTC

29

(2) INFORMATION FOR SEQ ID NO: 27:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

CCCGAATTCT GCTATGGTGC TGCCTGTG

28

(2) INFORMATION FOR SEQ ID NO: 28:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

CGCATCCAAA ACCGTACCTG TGCTGCCTGA

30

(2) INFORMATION FOR SEQ ID NO: 29:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

TTTATCACTT TCCGGGGGCA GGAGCGGAAT

30

(2) INFORMATION FOR SEQ ID NO: 30:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

GTTGGAACAG CAGACAGCGG TTTGCGCCCC

30

10 (2) INFORMATION FOR SEQ ID NO: 31:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

GAACATACTT TGTCGTTTT TCGCGTCAA

30

20 (2) INFORMATION FOR SEQ ID NO: 32:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:
(A) ORGANISM: N. meningitidis
(B) STRAIN: IM2394

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

Tyr Lys Gly Thr Trp
1 5

30 (2) INFORMATION FOR SEQ ID NO: 33:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:
(A) ORGANISM: N. meningitidis
(B) STRAIN: IM2394

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

40 Glu Phe Glu Val Asp Phe Ser Asp Lys Thr Ile Lys Gly Thr Leu
1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: N. meningitidis
(B) STRAIN: IM2394

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

Glu Gly Gly Phe Tyr Gly Pro Lys Gly Glu Glu Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: N. meningitidis
(B) STRAIN: IM2394

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

Ala Val Phe Gly Ala Lys
1 5

(2) INFORMATION FOR SEQ ID NO: 36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2070 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Neisseria meningitidis
(B) STRAIN: BZ83

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: 1..60

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
(B) LOCATION: 61..2067

(ix) FEATURE:

- (A) NAME/KEY: CDS
(B) LOCATION: 1..2067

ATGAACAATCCATTGGTAAATCAGGCTGCTATGGTGCTGCCTGTGTTTTGTTGAGTGCT 50
TACTTGTTAGGTAACCAATTTASTCCGACGATACCACGACGGACACAAAAACAACTCACGA
MetAsnAsnProLeuValAsnGlnAlaAlaMetValLeuProValPheLeuLeuSerAla

TGTCTGGGCGGAGGCGGCASITTCGATCTTGAATCTGTGATACCGAAGCCCCGCGTCCC 120
ACAGACCCGCTCCGCCGTCAAAGCTAGAACTAAGACAGCTATGGCTTCGGGGCGCAGGG
CysLeuGlyGlyGlyGlySerPheAspLeuAspSerValAspThrGluAlaProArgPro

GCGCCAAAGTATCAAGATGTTCTTCGAAACACCGCAAGCCCCAAAAAGACCAAGGCGGA 180
CGCGGTTTTCATAGTTCTACAAAGAGGCTTTGTGGCGTTCGGGTTTTTCTGGTTCCGCCT
AlaProLysTyrGlnAspValSerSerGluThrProGlnAlaGlnLysAspGlnGlyGly

TACGGTTTTTGCAATGCGCTTCAAGCGGCGGAATTGGTACCCAAAAAATGAAGAAGATCAT 240
ATGCCAAAACGTTACGCGAAGTTCGCCGCTTAACCATGGGTTTTTACTTCTTCTAGTA
TyrGlyPheAlaMetArgPheLysArgArgAsnTrpTyrProLysAsnGluGluAspHis

AAGGCATTATCAGAAGCGGATTGGGAGAAGTTAGGTGCGGTAAGCCAGATGAGTTTCCC 300
TTCCGTAATAGTCTTCGCCTAACCTCTTCAATCCACGCCCAATTCGGTCTACTCAAAGGG
LysAlaLeuSerGluAlaAspTrpGluLysLeuGlyAlaGlyLysProAspGluPhePro

CAAAGGAATGAAATATTGAATATGACTGACGGAATTCTGAGTGAGTCTCTTCAGCTGGGT 360
GTTTCCTTACTTTATAACTTATACTGACTGCCCTTAAGACTCACTCAGAGAAGTCGACCCA
GlnArgAsnGluIleLeuAsnMetThrAspGlyIleLeuSerGluSerLeuGlnLeuGly

GAGGGCGGGCAAAAGCCGCGTAGAAGGATACACGGATTTCCTCATATGTCCGCTCGGGCTAT
-----+
CTCCGCGCGTTTTCGGCGCATCTTCCTATGTGCCTAAAGGTTATACAGGGCGAGCCCGATA 420

GluGlyGlyLvsSerArgValGluGlyTyrThrAspPheGlnTyrValArgSerGlyTyr

ATCTACCGCAACGGTGGCAATAAAATCGATTTCGAAAAAAATCGCCCTTTCCGGTCCG
-----+ 480
TAGATGGCGTTGCCACGGTTATTTTAGCTAAGGT.TTTTITAGCGGGAAAGGCCAGGC
IleTyrArgAsnGlnAlaAsnLysIleAspPheGlnLysLysIleAlaLeuSerGlyPro

GACGGCTACCTTTTCTACAAAGGCAGCAATCCTTCCCAAGCTCTGCCGATGGGTAAGGTA
 -----+ 540
 CTGCCGATGGAAAGATGTTTCCCTCGTTAGCAAGGGTTCGAGACGGCTACCCATTCCAT
 AspGlyTyrLeuPheTyrLysGlySerAsnProSerGlnAlaLeuProMetGlyLysVal

GTTTATAAAGGTACTTGGGATTATGTAACCGATGCCAAGATGGGCACAAAATTTTCCAG
-----+-----+-----+-----+-----+-----+-----+
CCAATATTTCATGAACCTAATACATTGGCTACGGTCTACCCTGTTTTTAAAGGGTC

600

Gly Tyr Lys Gly Thr Trp Asp Tyr Val Thr Asp Ala Lys Met Gly Gln Lys Phe Ser Gln

TTGGCTGCTTTTCCAGCGGGGGATAGGTATGGGGCTTTGTCTGCCGAGGAAGCGGATGTG
 -----+ 660
 AACCGACCAAAGGTGCGCCCCCTATCCATACCCCGAAACAGACGGCTCCTTCGCCTACAC
 LeuAlaGlyPheProAlaGlyAspArgTyrGlyAlaLeuSerAlaGluGluAlaAspVal

TTCGCGCAACAAAAGCGAGGCACAGCAAGGTCTAGACCGATTTCGGGCTGACCAGCGAGTTT
-----+-----+-----+-----+-----+-----+-----+-----+
AACGCGTTTGTTTTTCGCTCCGTGTCGTTCCAGTCTGGCTAAAGCCCAGACTGGTCGCTCAA

LeuArgAsnLysSerGluAlaGlnGlnGlyGlnThrAspPheGlyLeuThrSerGluPhe

GAGGTGGATTTCGCGCCAAGACCATGACCGCGCGGCTCTACCGCAATAACCGGATTACT
-----+ 780
CTCCACCTAAAGCGSCGGTTCTGGTACTGGCCGCGCGAGATGSCGTTATTGGCCTAATGA
GluValAspPheAlaAlaLysThrMetThrGlyAlaLeuTyrArgAsnAsnArgIleThr

GCCCAACTGGTTGTCGACGGCATTATGATTCCGCTCCTSCCCAGAAATTCGAAAGCGAG 1260
CGGGTTGACCAACAGCTGCCGTAATACTAAGGCGAGGACGGGTTCTTAAGGCTTTCGCTC
AlaGlnLeuValValAspGlyIleMetIleProLeuLeuProLysAsnSerGluSerGlu
-----+-----
AGCAATCAGGCAGATAAAGGTAAAAACGGCGGAACAGCCTTTACCCGCAAATTTGAACAC 1320
TCGTTAGTCCGTCTATTTCCTATTTGCGGCTTGTCCGAAATGGGCGTTTAAACTTGTG
SerAsnGlnAlaAspLysGlyLysAsnGlyGlyThrAlaPheThrArgLysPheGluHis
-----+-----
ACGCCGGAAGTGATAAAAAAGACACCCAAAGCAGGTACGGCGGAGAATGGCAATCCAGCC 1380
TGCGGCTTTCACCTATTTTCTGTGGGTTCCGTCCATGCCGCTCTTACCGTTAGGTCGG
ThrProGluSerAspLysLysAspThrGlnAlaGlyThrAlaGluAsnGlyAsnProAla
-----+-----
GCTTCAAATACGGCAGGTGATACCAATGGCAAAACAAAAACCTATGAAGTCGAAGTCTGC 1440
CGAAGTTTATGCCGTCCACTATGGTTACCGTTTTGTTTTTGGATACTTCAGCTTCAGACG
AlaSerAsnThrAlaGlyAspThrAsnGlyLysThrLysThrTyrGluValGluValCys
-----+-----
TGTTCCAACCTCAATTATCTGAAATACGGAATGTTGACGCGTAAAAACAGCAAGTCCGCG 1500
ACAAGGTTGGAGTTAATAGACTTTATGCCTTACAACTGCGCATTTTGTCTGTTTCAGGCGC
CysSerAsnLeuAsnTyrLeuLysTyrGlyMetLeuThrArgLysAsnSerLysSerAla
-----+-----
ATGCAGGCAGGCGAAAACGGTAGTCTAGCTGACGCTAAAACGGAACAAGTTGAACAAAGT 1560
TACGTCGGTCCGCTTTTGCCATCAGATCGACTGCGATTGTGCTTCAACTTGTTCATCA
MetGlnAlaGlyGluAsnGlySerLeuAlaAspAlaLysThrGluGlnValGluGlnSer
-----+-----
ATGTTCTCTCAAGGCGAGCGCACCGATGAAAAAGAGATTCCAAAAGAGCAACAAGACATC 1620
TACAAGGAGGTTCCGCTCGCGTGGCTACTTTTCTCTAAGGTTTCTCGTTGTTCTGTAG
MetPheLeuGlnGlyGluArgThrAspGluLysGluIleProLysGluGlnGlnAspIle

GTTTATCGGGGGTCTTGGTACGGGCATATGCCAACGACACAAGCTGGAGCGGCAATGCT
 -----+ 1680
 CAAATAGCCCCCAGAACCATGCCCGTATAACGGTTGCTGTGTTGACCTCGCCGTTACGA
 ValTyrArgGlySerTrpTyrGlyHisIleAlaAsnAspThrSerTrpSerGlyAsnAla

TCAGATAGAGAGGGCGGCAACAGGGCGGACTTTACCGTGAATTTTGGTACGAAAAAAATT
----- 1740
AGTCTATCTCTCCGCGGTGTCCCGCTGAAATGGCACTTAAACCATGCTTTTTTTTAA
SerAspArgGluGlyGlyAsnArgAlaAspPheThrValAsnPheGlyThrLysLysIle

~~AACGGAACTTAACCGCTGAAAACAGGCAGGAGGCCAACCTTTACCATTGTGGGCGATATT~~
-----+-----+
~~TTCCTTGCAATTGGCGACTTTTTGTCCTCCTCCGTTGGAAATGGTAAACCCGCTATAA~~

AsnGlyThrLeuThrAlaGluAsnArgGlnGluAlaThrPheThrIleValGlyAspIle

AAGGACAACGGCTTTGAAGGTACGGCGAAAACTGCTGACTCAGGTTTTGATCTCGATCAA
-----+-----+-----+-----+-----+-----+-----+-----+-----+
TTCCTGTTGCCGAAACTTCCATGCCGCTTTTGAGGACTGAGTCCAAAAGTAGAGCTAGTT

LysAspAsnGlyPheGluGlyThrAlaLysThrAlaAspSerGlyPheAspLeuAspGln

~~AGCAATACCA~~~~CCCGCACG~~~~CCTAAGGC~~~~TATATC~~~~ACAGATGC~~~~CAAGGTGA~~~~AGGGCGGTTT~~
-----+-----+
~~TCGTTATGGT~~~~GGGCGTG~~~~CGGATTCC~~~~GATATAGT~~~~GTCTACGG~~~~ATCCACTT~~~~CCCCGCCAAA~~

SerAsnThrThrArgThrProLysAlaTyrIleThrAspAlaLysValLysGlyGlyPhe

TACGGGCGCTAAAGCCGAAGAGTTGGGCGGATGGTTTGCTATCCGGGCGATAAACAAACG
-----+-----+ 1980
ATGCCCGGATTCGGCTTCTCAACCCGCTACCAAACGGATAGGCCCGCTATTGTGTTGC
TyrGlyProLysAlaGluGluLeuGlyGlyTrpPheAlaTyrProGlyAspLysGlnThr

GAAAAGGCAACGTTACATCGGGCGATGGAAATTCAGCAAGCAGTSCAACTGTCGTATTTC
CTTTTCGGTTGCCAATGTAGGCCGCTACCTTTAAGTCGTTTCGTCACGTTGACAGCATAAG 2040
GluLysAlaThrValThrSerGlyAspGlyAsnSerAlaSerSerAlaThrValValPhe

GGTGCGAAACGCCAAAGCCTGTGCAATAA 2070
CCACGCTTTGCGGTTTCGGACACGTTATT
GlyAlaLysArgGlnLysProValGlnTer

INFORMATION FOR SEQ ID NO: 37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 669 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

(2) INFORMATION FOR SEQ ID NO: 38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2136 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria meningitidis*
(B) STRAIN: BZ163

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: 1..60

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
(B) LOCATION: 61..2133

(ix) FEATURE:

- (A) NAME/KEY: CDS
(B) LOCATION: 1..2133

ATGAACAATCCATTGGTAAATCAGGCTGCTATGGTGGTGCCTGTGTTTGTGAGTGCT 60
TACTTGTAGGTAACCATTTAGTCCGACGATACCACGACGGACACAAAAACAATCAGCA
MetAsnAsnProLeuValAsnGlnAlaAlaMetValLeuProValPheLeuLeuSerAla

TGTTTGGGCGGAGGCGGCAGTTTCGATCTTGATTCTGTGATACCGAAGCCCCGCGTCCC 120
ACAAACCCGCTCTGCGCTCAAGCTAGAACTAAGACAGCTATGGCTTCGGGGCGCAGGG
CysLeuGlyGlyGlyGlySerPheAspLeuAspSerValAspThrGluAlaProArgPro

GCGCCAAATATCAAGATGTTCTTCGAAAAACCGCAAGCCCCAAAAGACCAAGGCGGA 180
CGCGGTTTTATAGTTCTACAAAGAGGCTTTTTGGCGTTCGGGTTTTCTGGTTCGCGCT
AlaProLysTyrGlnAspValSerSerGluLysProGlnAlaGlnLysAspGlnGlyGly

TACGGTTTTGCGATGAGGTTGAAACGGAGGAATCGGCATCCGCAGGCAAAAGAAGACAAA 240
ATGCCAAAACGCTACTCCAACCTTGCCCTCTTAGCCGTAGGCGTCCGTTTTCTTCTGTT
TyrGlyPheAlaMetArgLeuLysArgArgAsnArgHisProGlnAlaLysGluAspLys

GTTGAACTAAACCCAAATGATTGGGAGGAGACAGGATTGCCGAGCAAGCCCCAAACTTA 300
CAACTTGATTGCGTTTACTAACCCTCCTCTGTCTTAACGGCTCGTTTCGGGGTTTTGAAT
ValGluLeuAsnProAsnAspTrpGluGluThrGlyLeuProSerLysProGlnAsnLeu

CCCGAGCGACAGCAATCGGTTATTGATAAAGTAAAAACAGACGATGGCAGCAATATTTAC 360
GGGCTCGCTGTCGTTAGCCAATAACTATTTCATTTTGTCTGCTACCGTCGTTATAAATG
ProGluArgGlnGlnSerValIleAspLysValLysThrAspAspGlySerAsnIleTyr

ACTTCCCCCTATCTCAGCCAAATCAAACCTCAAAACGGCAGCAGCTAATAGCGGTGCAAAC 420
TGAAGGGGAATAGAGTGCCTTAGTTTGGTAGT.TTTCGCCCTCGTGATTATCGCCACGTTTG
ThrSerProTyrLeuThrGlnSerAsnHisGlnAsnGlySerThrAsnSerGlyAlaAsn

CAACCAAAACCAAGTAAAGATTACAAAATTTCAAATATGTTTATTCGGGCTGGTTT 480
GTTGGTTT.TTTCGCTCATTTTCTAATGTTTAAAGTTTATACAAATAAGGCCGACCAAA
GlnProLysAsnGluValLysAspTyrLysAsnPheLysTyrValTyrSerGlyTrpPhe

TATAAACATGCAGAGAGTGAAGAGAAATTCAGTAAATCAAATTTAAGTCAGGCCGACGAC 540
ATATTTGTACCTCTCTCAC.TTTCCTTAAGTCATTTTAGTTTAAATTCAGTCCGCTGCTG
TyrLysHisAlaGluSerGluArgGluPheSerLysIleLysPheLysSerGlyAspAsp

GGCTATATTTTTTATCACGGTAAAGACCCTTCCCGACAACCTCCCACTTCTGAAAAAGTT 600
CCGATATAAAAAATAGTGCCATTTCTGGGAAGGGCTGTTGAAGGGTGAAGACTTTTTCAA
GlyTyrIlePheTyrHisGlyLysAspProSerArgGlnLeuProThrSerGluLysVal

ATCTACAAAGGCGTATGGCATTITGTAAACCGATACTGAAAAGGGACAAAATTTAACGAT 660
TAGATGTTTCCGCATACCGTAAACATTGGCTATGACTTTTCCCTGTTTTTAAATGCTA
IleTyrLysGlyValTrpHisPheValThrAspThrGluLysGlyGlnLysPheAsnAsp

ATTCTTGAAACCTCAAAAGGGCAAGGCGACAGATACAGCGGATTTTCGGGCGATGACGGC 720
TAAGAACTTTGGAGTTTTCCCGTTCGGCTGTCTATGTCGCCTAAAAGCCCGCTACTGCCG
IleLeuGluThrSerLysGlyGlnGlyAspArgTyrSerGlyPheSerGlyAspAspGly

GAAACAACCTTCCAATAGAACTGATTCCAACCTTAATGATAAGCACGAGGGTTATGGTTTT 780
CTTTGTTGAAGSTTATCTTGACTAAGGTTTGAATTACTATTTCGTGCTCCCAATACCAAAA
GluThrThrSerAsnArgThrAspSerAsnLeuAsnAspLysHisGluGlyTyrGlyPhe

ACCTCGAATTAGAAATGGATTTCGGCAGTAAAAATTCACGGGTAAATTAATACGCAAT

TGGAGCTTAAATCTTCACCTAAAGCCCTCAATTTAACTGCCCATTTAATTATGCGTTA 840
ThrSerAsnLeuGluValAspPheGlySerLysLysLeuThrGlyLysLeuIleArgAsn

AATAGAGTTACAAACGCTACTACTAACGATAAATACACCACCCCAATACTACAGCCTTGAT

TTATCTCAATGTTTGGGATGATGATTGCTATTTATGTGTTGGGTTATGATGTCCGAACTA 900
AsnArgValThrAsnAlaThrThrAsnAspLysTyrThrThrGlnTyrTyrSerLeuAsp

GCCCCAATAACAGGCAACCGCTTCAACGGTAAGGCGATAGCGACCGACAAACCCGACACT

CGGGTTTATTGTCCGTTGGCGAAGTGGCCATTCGCTATCGCTGGCTGTTTGGGCTGTGA 960
AlaGlnIleThrGlyAsnArgPheAsnGlyLysAlaIleAlaThrAspLysProAspThr

GGAGGAACCAAACACTACATCCCTTTGTTCCGACACGTCCTTCTTGAGCGGCGGCTTTTTTC

CCTCCTTGTTTGTATGTAGGGAAACAAAGGCTGAGGAGAAGAACTCGCCGCCGAAAAAG 1020
GlyGlyThrLysLeuHisProPheValSerAspSerSerSerLeuSerGlyGlyPhePhe

GGTCCGAAGGGTGAGGAATTGGGTTTCCGCTTTTTGAGCGACGATAAAAAAGTTGCGGTT

CCAGGCTTCCCACTCCTTAACCCAAAGCGGAAAAACTCGCTCCTATTTTCAACGCCAA 1080
GlyProLysGlyGluGluLeuGlyPheArgPheLeuSerAspAspLysLysValAlaVal

GTCGGCAGCGCGGAAAAACCAAGACAAAACGGAAAAATGGCGGGTGGCTTCAGGTGGCACA

CAGCCGTCGGCGCTTTGGTTTCTGTTTGCCTTTACCGCGCCACCGAAGTCCGCGGTGT 1140
ValGlySerAlaLysThrLysAspLysThrGluAsnGlyAlaValAlaSerGlyGlyThr

GATGCGGCAGCATCAAAACGGTCCGGCAGGCGAGCTGGTTCGAAAACAGTAAGCTGACCACG
CTACGCCGTCGTAGTTTCCACGCCGTCCTGCAGCAGACTTTGTCATTGCACTGGTGC
AspAlaAlaAlaSerAsnGlyAlaAlaGlyThrSerSerGluAsnSerLysLeuThrThr

GTTTCGATGCGGTCCAGCTGAAATTGGGCGATAAGGAAGTCCAAAAGCTCGACAACCTTC
CAAAACCTACGCCAGCTCGACTTAACCCGCTATTCTTCAGGTTTCGAGCTGTTGAAG
ValLeuAspAlaValGluLeuLysLeuGlyAspLysGluValGlnLysLeuAspAsnPhe

AGCAACGCCGCCCAACTGGTTGTCGACGGCATTATGATTCCGCTCTTGCCCGAGACTTCC
TCGTTGCGGCGGGTTGACCAACAGCTGCCGTAACTAAAGGCGAGAACGGGCTCTGAAGG
SerAsnAlaAlaGlnLeuValValAspGlyIleMetIleProLeuLeuProGluThrSer

GAAAGTGGGAACAATCAAGCCAATCAAGGTACAAATGGCGGAACAGCCTTTACCCGCAA
CTTTCACCCCTTGTTAGTTCGGTTAGTTCCATGTTTACCGCCTTGTCGGAAATGGGCGTTT
GluSerGlyAsnAsnGlnAlaAsnGlnGlyThrAsnGlyGlyThrAlaPheThrArgLys

TTTGACCACACGCCGGAAGTGATAAAAAAGACGCCCAAGCAGGTACGCAGACGAATGGG
AAACTGGTGTGCGGCCCTTCACTATTTTTCTSCGGGTTGTCATGCGTCTGCTTACCC
PheAspHisThrProGluSerAspLysLysAspAlaGlnAlaGlyThrGlnThrAsnGly

GCGCAAACCGCTTCAAATACGGCAGGTGATACCAATGGCAAAACAAAAACCTATGAAGTC
CGCGTTTGGCGAAGTTTATGCCGTCCTACTATGTTACCGTTTGTGTTTGGATACTTCAG
AlaGlnThrAlaSerAsnThrAlaGlyAspThrAsnGlyLysThrLysThrTyrGluVal

GAAGTCTGCTGTTCCACCTCAATTATCTGAAATACGGAATGTTGACGCGCAAAAACAGC
CTTCAGACGACAAGGTTGAGTTAATAGACTTTATGCCCTTACAACCTSCGCGTTTTTGTGCG
GluValCysCysSerAsnLeuAsnTyrLeuLysTyrGlyMetLeuThrArgLysAsnSer

AAATCCGCGATGCAGGCAGGAGAAAGCAGTAGTCAGCTGATGCTAAAAACGGAACAAAGTT
.....+
TTCAGGCGCTACGTCGGTCCTCTCTTCGTCATCAGTTCGACTACGATTTTGCCTTGTTCAA
LysSerAlaMetGlnAlaGlyGluSerSerSerGlnAlaAspAlaLysThrGluGlnVal
.....+
1520

GGACAAAGTATGTTCTTCCAAAGGCGAGCGCACCGATGAAAAAGAGATTCCAAGCGAGCAA
.....+
CCTGTTTCATACAAAGGAGGTTCGGCTCGCGTGGCTACTTTTCTCTAAGGTTTCGCTCGTT
GlyGlnSerMetPheLeuGlnGlyGluArgThrAspGluLysGluIleProSerGluGln
.....+
1680

AACATCGTTTATCGGGGGTCTTGGTACGGGCATATTGCCAGCAGCACAAAGCTGGAGCGGC
.....+
TTGTAGCAAATAGCCCCAGAACCATGCCCGTATAACGGTCGTCGTGTTTCGACCTCGCCG
AsnIleValTyrArgGlySerTrpTyrGlyHisIleAlaSerSerThrSerTrpSerGly
.....+
1740

AATGCTTCTGATAAAGAGGGCGGCAACAGGGGGAATTTACTGTGAATTTTGGCGAGAAA
.....+
TTACGAAGACTATTTCTCCCGCGTTGTCCCGCTTAAATGACACTTAAACCGCTCTTT
AsnAlaSerAspLysGluGlyGlyAsnArgAlaGluPheThrValAsnPheGlyGluLys
.....+
1800

AAAATTACCGGCACGTTAACCGCTGAAAACAGGCAGGAGGCAACCTTTACCATTGATGGT
.....+
TTTAATGGCCGTGCAATTGGCGACTTTTGTCCGTCTCCGTTGAAATGGTAACCTACCA
LysIleThrGlyThrLeuThrAlaGluAsnArgGlnGluAlaThrPheThrIleAspGly
.....+
1860

AAGATTGAGGGCAACGGTTTTTCCGGTACGGCAAAACTGCTGAATTAGGTTTGTATCTC
.....+
TTCTAACTCCCGTTGCCAAAAAGGCCATGCCGTTTTTGACGACTTAATCCAAACTAGAG
LysIleGluGlyAsnGlyPheSerGlyThrAlaLysThrAlaGluLeuGlyPheAspLeu
.....+
1920

GATCAAAAATAACACCCGACGCGCTAAGGCATATATCACAGATGCCAAGGTGCAGGGC 1980
CTAGTTTTTTTATGGTGGGCGTGCGGATTCGGTATATAGTGTCTACGGTTCCACGTCCCG
AspGlnLysAsnThrThrArgThrProLysAlaTyrIleThrAspAlaLysValGlnGly

GGTTTTTACGGGCCCCAAGCCGAAGAGTTGGGCGGATGGTTTTGCCTATCAGGGCGATAAA 2040
CCAAAAATGCCCGGGTTTCGGCTTCTCAACCCGCTACCAAACGGATAGTCCCGCTATTT
GlyPheTyrGlyProLysAlaGluGluLeuGlyGlyTrpPheAlaTyrGlnGlyAspLys

CAAACGGAAAATACACAGTTGCATCCGCGCAATGGAAATTCAGCAAGCAAGTGCAACTGTC 2100
GTTTGCCTTTTATGTTGTCAAGCTAGGCGCTTACCTTTAAGTCGTTTCGTCACGTTGACAG
GlnThrGluAsnThrThrValAlaSerGlyAsnGlyAsnSerAlaSerSerAlaThrVal

GTATTCGGTGCAGAAACGCCAAAAGCCTGTGCAATAA 2136
CATAAGCCACGCTTTGCGGTTTTTCGGACACGTTATT
ValPheGlyAlaLysArgGlnLysProValGlnTer

INFORMATION FOR SEQ ID NO: 39:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 692 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39: